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GenCore version 5.1.3
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UM protein - protein search, using sw model

Pun on:

January 28, 2003, 11.43:11, Search time 39 Seconds (without alignments) 1387.173 Million cell updates/sec

US-09-828-432-3 Perfect score: QPNPPIPWEHEDQETGEGVK

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 MNVSFAHLHFAGGYLPSDSQ. Scoring table:

Sequence:

908470 segs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 2ουοορορο Minimum DB Maximum DB

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

| SIDS2/gagdata/geneseq_geneseq_embl/AA1999.DAT:
| SIDS2/gagdata/geneseq_geneseq_embl/AA1990.DAT:
| SIDS2/gagdata/geneseq_geneseq_embl/AA1991.DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1		p (
resurc		Onery				
No.	Score	Match	Match Length DB	DB	ID	Description
1	2167	100.0	406	23	AAU98047	Himman HGBRBMV7 N.+
2	23.67	100.0		23	AAU98048	Human HGDRBMV7
3	2167	100 D		23	ABG61638	Human G protein-co
4	2167	100.0		23	AAU10631	Novel G-protein on
2	2167	100.0	419	22	AAII08807	Galanin recentor-1
9	2167	100.0		22	AAE06761	Himan Gentotein oo
7	2167	100.0		1 2	AAG63344	Amino acid semiono
8	2167	100.0		CI CI	AA1104363	Himan G-raylein
6	2167	100.0		22	AAU01848	Human DNA Genrotes
10	2167	100 0	419	22	AAB60691	Human G protein-co

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AAU1063	AAE1708	AAG6334	AAG6412	AAU7324	AAU9790	AAUSSES	ABG6164	AAW6146	AAWE133	AAW490	AAU7454	AAT4512	AABE513	AAG6821	AAW4013	AAW2456	AAW6138	AAW4900	AAW6146	AAWEZZZ	AAW4013	AAY4513	AAB6513	AAU7454	AAG6821	AAY 065	AAW5225	AAW2456	AAW6146	AAW6138	AAW4900	AAU7454	AAR9506	AAR9122
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ALIGNMENTS

AAU98047 standard, Protein, 406 AA 13-AUG-2002 (first entry) AAU98047; RESULT 1 AAU98047

Human HGPRBMY7 N-terminal deletion mutant representative sequence

Human; G protein-coupled receptor; HGPRBMY7; spinal chord; spinal chord-related disorder; breast cancer; neoplastic disease; brain disorder; leukaemia; myeloma; immunological disorder; cholecystitis; Grave's disease; osteoarthritis; asthma, neurological disorder; dementia; depression; Alzheimer's disease; Down's syndrome; epilepsy; intracellular calcium level; NFAT; nuclear factor activator of transcription element; mutant; mutann.

Homo sapiens. Synthetic. Location/Qualifiers Misc-difference 1..399

(notes "The Noterminus can be optionally and sequentially deleted by one amino acid at a time"

WO200226823-A2

04-APR-2002

26-SEP-2001; 2001W9-US30351.

27-SEP-2000; 2000US-235731P.

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The invention relates to an isolated polypeptide (1) comprising amino acid sequence that is at least 96% identical to a polypeptide fragment of a fully defined human of precision coupled receptor BMY? (HoppeMY) proposed on variant, allelic variant or species homologue.

Also included are polymicleotides encoding the above polypeptides, or variant states are useful for diagnosis prevention, treating or ameliorating a medical condition e.g. a disease, disorder, or a condition related to brain, breast, gastroinfestinal or erebellum, candate nucleus, and disorder related disorders, hippocampus, brain, breast, colon, spinal chord-related disorders, hippocampus, brain, breast, colon, spinal chord-related disorders, bippocampus, brain, breast, colon, spinal chord-related disorders, colondand and brain. An antagonist or inhibitor of (1) identified using (1) is useful for treating a neoplastic disorder such as leukaemia, myeloma, immunichgical disorders such as dementia, depression, Alzheimer's disease, nown's syndrore and epilepsy.

HOPPEMY, its polymoleotide and agonists or antagonists of the colondarial and agonists or antagonists of the
                                                                                                                                                                                                                                                                                                                                                                                    Howel humin 5 protein complet reseptor PMT2 (HoppBMT2) polypeptide, useful for modulators of HGPRBMY2 activity that are useful for treating leukaemia, cholecystitis, Grave's disease, epilepsy, dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide are useful for modulating intracellular calcium levels, modulating Caloia levels, modulating Caloia sensitive signalling pathways and modulating nuclear factor activator of transcription (NFAT) element associated signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HSLILNISLADLSLLLFSAPIPATAYSKSVWDLGWEVCKSSPWFIHTCMAAKSLTIVVVA 120
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                                                                                                                                                                                          Feder JN, Mintier G, Ramanathan CS, Westphal R; cane A, Barber L, Kornacker MG;
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                                                                                                                 (RRIM ) BRISTOL-MYERS SQUIBE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Fig 2; 170pp; English
14-FEB-2001; 2001US-268580P.
28 AUG Jeal; 2201US-215423F.
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/notes "The C-terminus can be optionally and sequentially
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                                                                                                                                   Human HGPRBMY7 C-terminal deletion mutant representative sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feder JN, Mintier G, Ramanathan TT,
                                                                                                                                                                                                                                                                                                                 deleted by one amino acid at a time"
361 KTEFAELIIIPPOVEQFWHEEDIVIOVQUODFIFWHHIGHIGHTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cacace A, Barber L, Kornacker MG;
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                   AAU98048 standard, Protein, 406 AA
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                                                                                                                                                                                                                                                                                                                                                                                                        27.SEP-2000; 2000US 235731P.
                                                                                                                                                                                                                                                                                                                                                                                                                  14 FEB 2001; 2001US 268580P.
28-AUG-2001; 2001US-315423P.
                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-2001; 2001WO-US30351
                                                                                                              13-ATS-2012 (first entry)
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                                                                                                                                                                                                                                                   sapiens.
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                                                                                                                                                                                                                                                            Synthetic
                                                                                         AAUGRO48;
                                             RESULT 2
AAU98048
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The invention relates to an inclated polypoptide of the product that is a clear 95% identical to a polypoptide that is at least 95% identical to a polypoptide that is at least 95% identical to be produced to the polypoptide, or variant, allelic variant or species benedonus.

As included that is provided to the properties benedonus. As a factor of the properties of the p chord and brain. An antagonist or inhibitor of (1) identified using (i) is useful for treating a reaplicity discribe or 4 or 5.5 km m. 79 km m, immunological disorders such as cholecystifts, thave's thavase, content title, at them, realizable of first despite as decembered depression, Alzhaimer's disease, Down's syndicme and entires.

HGPREMY7, its polymunologide and aponicts or antagonists of the Novel human G-protein coupled receptor HMY7 (HGPFPMY3) pripperies, useful for modulating of HGFPMY3 and Mily that are useful for the annual cukaemia, cholegystitis, Grave's disease, epilepsy, dementation Claim 12, Fig 2, 170pp, English. depression

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300

A 1 FTEYAFIPILPNVEQFWHEPDTVPSVQNNGPIPWEHENQETGEVV 406

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                  modulating Ca^2+ sensitive signalling pathways and modulating nuclear factor activator of transcription (NFAT) element associated signalling pathways. The present sequence is a representative sequence for a set of sequential C-terminal deletion mutants of HGPRBMY?
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polypeptide are useful for modulating intracellular calcium levels,
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                                                                                                                                                                       Score 2167; DB 23; Length 406; Pred. No. 2.5e-191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Down's syndrome; epilepsy; intracellular calcium level; NPAT;
nuclear factor activator of transcription element.
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                                                                                                                                                                                                                 0; Mismatches
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-FEB-2001; 2001US-268580P.
AUG 2001; 2001US-315423P.
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                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 406; Conservative
                                                                                                                              406 AA,
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                                                                                                                                Sequence
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14-FEB-
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The invention relates to an isolated polypeptide (IV comprising amino acid sequence that is at least 95% identical to a polypeptide fragment of acid sequence that is at least 95% identical to a polypeptide fragment of properties, or variant, alselic variant or species homologue.

Also included are polymucleotides encoding the above polypeptides, as a pression vectors, host cells, anti-HGPRBWY7 antibodies and modulators of HGPRBWY7. HGPRBWY7 and its polymucleotide are useful for diagnosis prevention, treating or ameliorating a medical condition e.g. a disease, disorder, or a condition related to brain, breast, gastrointestinal or musculo-skeletal systems, such that thalamuse, compus callosum, caudate nucleus, amygdala, substantia nigra.

Cerebellum, caudate nucleus, amygdala, substantia nigra, brain, breast, colon, spinal chord-related to spinal breast cancer, neoplastic diseases, and disorders related to spinal chorder and brain An antagonist or inhibitor of [1] identified using [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is useful for treating a neoplastic disorder such as leukaemia, myeloma, immunological disorders such as cholecystitis, Grave's disease, ostboarders such as dementia, dependentitis, asthma, neurological disorders such as dementia, depression, Alaheimer's disease, Down's syndrome and epilepsy. HGPRBMY7, its polynucleotide and agonists or antagonists of the polypeptide are useful for modulating intracellular ralcum invels, modulating Ca<sup>2</sup>, sensitive signalling pathways and modulating nuclear factor activator of transcription (DRAT) element associated signalling pathways. The present sequence is the HGPRBMY7 protein sequence.
                                                                                                                                                  Novel human G.protein coupled receptor EMY7 (HGPREMY7 pclypoptide, useful for modulators of HGPREMY7 activity that are useful for iresting leukacmia, cholecystitis, Grave's disease, epilepsy, dementia, depression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VAEERSMESSELFELARGLELBFASETFWRAYTOCFFFFOUTOU FULLEFFFCTTVALL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2167; DB 23; Length 406; 100.0%; Pred. No. 2.5e-191; tive 0; Mismatches 0; Indels 0;
Mintier G, Ramanathan CS, Westphal
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                   Barber L, Kornacker MG;
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Matches 406; Conservative (
Feder JN,
                      Cacace A,
                                                                            WPI; 2002-435195/46.
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Battaglino P,
                            Hawken DR,
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RESULT 4

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AAU10631 standard; Protein; 406 AA
                                                                                   (first entry)
                                                                                   05-JUN-2002
                                                 AAIII 0631:
AAU10631
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Novel G-profein coupled receptor 2017 (nopop-2017) version #2

d protein coupled receptor, GPCP-1037, human, antiinflammatory, immunoseggressive, cerebrogetive, tranguliser, anticenvulsant; montropic, neuroleptic, neuroperative, tranguliser, anticenvulsant; HIV, disheres, gressive, morals disperser, typicid disperser, renal failure, Crohn's disease, cell differentiation, homeostasis, movement disorder, GR disorder, stroke, Huntington's disease, fourtete's Syndrome, dyskinesia, attention disorder, movement disorder, degenerative disorder, Parkinson's disease, Alzheimer's disease; ataxia, expranuclar palsy, metabolic disorder, andiovascular disorder, annexal, hormonal disorder, pelycystic ovarian syndrome, alopecia.

Home sapiens

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/label- Transmembrane_domain_1
                                                                                 · Transmembrane_domain_2
                                                                                        label= Transmembrane_domain_3
                                                                                                      Transmembrane domain 5
                                                                                                             Transmembrane_domain_6
                                                                                               Transmembrane_domain_4
                                                                                                                    /label= Transmembrane_domain_7
                                                                    location/Qualifiers
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W0200177175 A2

18-0-1-2001

06-APR-2001; 2001WQ-US11331

08-APP 2000; 2000US 145224P 05-DEC-2000; 2000US-251313P.

(PHAA) PHARMACIA & UPJOHN CO.

Berthold M; Sejlitz T, Vogeli G, Lind P,

WPI; 2002 017449/02. N-PSDB; AAS16253. Polymurlearide encoding novel G protein-coupled receptor-2037 and polypeptide useful for identifying modulators useful for treating disorders such as autoimmune disorders, stroke, diabetes, cancer, aloperia, anorexia

Claim 31; Page 61; 101pp; English

compound modulating activity preferably neuropeptide binding or signalling of [11] and for purifying a 9 protein from a sample containing the G protein. The polymucleotide [1] is useful for identifying a compound which binds to [1] encoding [11] and for identifying an animal homologue of [11] The method comprises DNA hybridisation or computer homology searches to identify notein and sequences of the animal that are homologous to [1]. The compounds identified by the screening methods The invention describes the novel isolated G-protein coupled receptor protein-2017. The polypectide (II) is useful as a vacine in a manmal against (IIV) for identifying a compound binding to (IIV) proforably compounds useful for treating mental disorders; for identifying a

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failure, inflammatory conditions of Crohn's disease, diseases related to cell differentiation and homessissis, Theusated and All Standard and Alsorders, CDA disorders, SA disease or Tourette's Syndrom, it'est in listadon, and degenerative disorders such as Parkinson's, Alzhemen's, worment disorders, including ataxias, supramuelear palsy, infections caused by human immunodeficienty rither (HIV), or HIV),
                                                                                                                                                                                                                                                                                                        metabolic and cardiovascular dispasos and dispudórs o o 1990. Edudotoco
anorexia, proliferative dispasos and cancers, and hyporproliferative
are useful for treating disorders which include thyroud discribers, remai
                                                                                                                                                                                                                                                                                                                                                                                disorders such as psortasis, hormonal disorders configuration of systems syndrome, alopenta, among others. This is the amine and seperated to labelled may need 0 ps to in a region of the person need 0 ps to in a region of the person need of the inventor of the method of the inventor.
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406 AA; Sequence

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181 VAEBEMSMEGKLYPLLAFGLPLFFASFYFWPAYDQCKKPGTFTQNI PNQ 1 B C K QVTVMLL. 240
                                                                                                                                                                                                          121 KVCFMYASDPAFQVSIHNYTIMSVIJVAIWTVASIJPIPFWFFSTTFUHFFSVEMMTVEM 186
                                              1 MNVSFAHLHEAGHILDERGOOMFTIIPALGVAVTIVGENG TOTGTTT FVAKEGERM
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           Similarity
                       Matches 406;
 Query Match
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AAU08807 standard; Protein; 419 AA

AAU08807;

19-DEC-2001 (first entry)

Galanin receptor-like G protein coupled receptor

Galamin receptor-like G protein coupled receptor, aronoctro; antidiabetic; cardiovascular, antiasthmatic; moleculor, antideposium, varoriogic; poortopic; memorropic; antimigramo; tranquic, anti-gynamorphical, gene autorropic; patimylogical discident, anti-tun; metor corplinal; gene herbylogical discident autorium;

activity.

Homo sapiens.

W0200168843-A1.

20.9EP 2001

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galanin receptor-like G-protein coupled receptor for therapeutic purposes, useful for treating disease by gene therapy. A pharmaceutical composition described in the specification is useful for modulating the activity of the Galanin receptor-like GPCR in a pathophysiological disorder, selected from obesity, diabetes, cardiovascular disease, asthma, pain, depression, ischaemia, Alzheimer's disease, sleep disorder, migraine, anxiety and reproductive disorder. Specifically, the composition is useful for modulating the activity of the receptor in coupled is useful for modulating the activity of the receptor in information, motor coordination, modulation of dopaminergic activity and neuroendocrine function. This sequence is the Galanin receptor-like g protein coupled receptor described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 VAEERSMSMFGKIXPLLAPGLPEPEASFYFWRAYDQCKKFGTKTQNLRNQIPSKQVTVMLL 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 HSLILNLSLADLSLLLFSAPIRATAYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 KVCFMYASDPAKQVSIHNYTIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                       Reagent and methods of regulating a galanin receptor-like G protein coupled receptors and their regulation for therapeutic purposes e.g. treatment of hypotension and asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes novel reagents and methods of regulating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 MNVSFAHLHFAGGYLPEDSQDWFTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGKPSMI
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100 0%; Pred No. 2 6e-191;
ive 0; Mismatches 0; Indels 0;
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                                            L6-MAP-2000; 2000US-0189898
                                                               2000013-0210002
                                                                                         07-DEC-2000; 2000US-0251515.
15-MAP 2001; 2001WO-EP02929
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Best Local Similarity 100 C
Matches 406; Conservative
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                                                                  2000;
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361 KTEKAEIPILPDVEQFWHERDTVPSVQDNDPIPWEHEDQETGEGVK 406
                                               374 KTEKARIPILPDVEQEWHERDTVPSVQDNDPIPWEHEDQETGEGVK 419
                                                                                                                                                                         AAE06761 standard; Protein, 419 AA
                                                                                                                                                                                                                            AAE06761;
                                                                                                                         RESULT 6
                                                                                                                                                    AAE06761
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16-OCT-2001 (first entry)
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Human G-protein coupled receptor-11 (GCREC-11) protein.

Human; G-protein coupled receptor-11; GCREC-11; cytestatic; hepitotropic; virucide; antinflammatory; anticonvulsant; antiemetic; neuroprotective; nootropic; cerebroprotective; hypotensive; tranquilliser; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; pendasis; cancer; neurological disorder; stroke; Altherosclerosis; charactery disease; Parkinson's disease; cardiovascular disorder; epilepsy; hypercension; varioose vein; vasculitis; dysphagia; dysphagia; anorexia; gastrointestinal disorder; panorealitis; autoimmune disorder; Addisor, sifeses; cardiovascular disorder; Addisor, sifeses; cardiovascular disorder; Addisor, infection; trans, metabolic disorder; diabetes; obestiy; osteoporosis; transgenic animal; gene therapy.

Homo sapiens.

/label= 7_transmembrane_receptor_domain /label= 7_transmembrane_receptor_domain 41..61 /label= Transmembrane_domain Location/Qualifiers Domain Domain Domain

WO200157085-A2

09-AUG-2001

01-FEB-2001; 2001WO-US03455

02.FEB.2000; 2000US-0180093.

(INCY-) INCYTE GENOMICS INC.

.,

Yue H, Au Young J, Baughn MR,

WPI; 2001-488869/53. N-PSDB; AAD12954.

Novel isolated human G-protein coupled receptor useful for diagnosing, preventing and treating cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory and metabolic

Claim 1; Page 119-120; 138pp; English.

The present sequence is human G-protein coupled receptor-11 (3CREC-11 protein. The present invention relates to GCREC protein and mudleic acids encoding them. 3CREC protein, the against or antigonary acids encoding them. 3CREC protein, where the discretion of continuous associated with deressed expression or overexpression of functional GCREC in a patient, where the disorder is selected from cell proliferative disorders such as actific versions. Conteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis, and cancer, neurological disorders such as epilepsy, stroke, Alzhenmer's disoase, Huntington's disease, Parkinson's disease, cardiovascular disorders such as dysphagial, dyspeptial, anoreasis, gastro intestinal disorders such as dysphagial, dyspeptial, anoreasis, naucoa the manuodeficiency syndrome (AIDS), Addison's disoase, Crohn's disease, contections, viral, bacterial, fungal, parasitic, protozoal, helminthic infections, trawns and metabolic disorders such as diabetes. effects of exogenous compounds on the expression of GCREC sequences. GCREC cDNA is useful to create knock in humanised animals (pigs) or transgenic animals (mice or rats) to model human disease, for therapeutic or diagnostic purposes, for somatic or germline genetherapy, to generate hybridisation probes useful in mapping the naturally occurring genemic sequence, and in molecular biological

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Claim 1; Page 104-106; 115pp; Japaneso.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hRUP9. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                                                                                                                                                                                                                                                                                                                                                                                                                      Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 VAEEFMSMFGKLYPLLAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 SIAIISALLWI,PEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KUCFMYASDPAKQVSIHNYIIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 VAEBFMSMFGKLYPLLAFGLPLFFASFYFWPAYDQCKKPGTKTQNLRNQIRSKOVTVMLL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 SIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEF 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           inverse agonists or partial agonists for use as therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a human G-protein coupled receptor (GPCR),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%, Score 2167, DB 22; Length 419; 100.0%; Pred. No. 2.6e-191; tive 0, Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 91-92; 160pp; English.
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reproduction and sexual medicine, inflammation, cancer, tissue repair, dermatology, skin pigmentation, photoaging, frailty, osteoporosis, cardiovascular disease, gastrointestinal disease, antiinfection, allergy and respiratory disease, sensory organ disorders, sleep disorders
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                                                                                                                                                                                                                                                                                                                     chromosome 5; antibody; immunogen; signal transduction; obesity; disbetes, metabolic disease; neutological disease; psychotherapeutics; urogenital disease; reproduction; sexual medicine; inflammation; cancer; tissue repair; dermatology; skin pigmentation; photoaging; traility; osteoporosis; cardiovascula disease; gastrointestinal disease, antiinfection, allergy; respiratory disease; sensory organ disorder; sleep disorder; hair loss; mutein.
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                                                                                                                                                                                                                                                                                          Human; G-protein coupled receptor; PFI-001; mutant;
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ANCERS; Luman, G protein-complet receptor, 7TK receptor, follogies daller, suffection, viral: bacterial; fungal; proteocan HIV-1; infection, viral: bacterial; fungal; proteocan HIV-1; infection, viral: bacterial; fungal; proteocan HIV-1; bath, cache, distant, infects, unimary retention, souther beart fallor; hyperension; baperension; angina partoris; protein infects, increased, anxiery, artifical, protein in the relational disorder; distant disorder; depression; delinion, demential severe mental retendation, dystinesia, Parkinson's disease; Bintingian disorder, day Torrette's syndrome, game therapy, vaccine; drug screening; signal transduction;
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61 HSLILNLSLADLSLILFSAPIRATAYSKSVWDLGWFVCYSSDWFIHTCMAAKSLTIVVVA 120
                                                                                                                                         KVOEMYAGDPAKOVSIBNYTIMSVLVAIMTVACLLELPERFESTIFBHFGVEMCLVDVPA 180
                                                                                                                                                                                                              134 KUCEMYASDPAKQUSIHNYTIWCULVAIWTVASLLPI,PEWFFSTIPHHEGUEMCLVPVPA 193
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                                                                                                                                                                                                                                                                                                                                                               194 VABBEMSMEGKLYFLLAFGLELFFASEYFWFARTOOFFFSTFFTJALEAGIESFYQVTVMLL
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The invention relates to the human g protein decision of XX F4 and AXCR40, to WAR enrodust AXCR40 (AAPS994), and AXCR40 to WAR enrodust AXCR40 and AXCR40 to MAXCR40 
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AXOR40-specific antibodice are needed for purifying the AXOR40 protein of fragments their second conference assertable with the resting conditions assertable with the expression.
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No. 2.68 [9]; Concervation 0; Mismatches 0; Eules.
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Claim 1, Page 31, 39pp; English.
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RESULT 11 AAU10630

us-09-828-432-3.rag

AAU10630 standard; Protein; 419 AA

AAU10630;

(first entry) 05-JUN-2002 Novel G-protein coupled receptor 2037 (nGPCR-2037) version #1.

G-protein coupled receptor, GPCR-2037, human, antinflammatory; immunosuppressive, cerebroprotective; tranquiliser; anticonvulsant; mostropic, neuroprotective, human immunodeficiency virus; HIV; diabetes; cytostatic; mental disorder; thyroid disorder; renal failure; Crohn's disease; cell differentiation; homeostasis; movement disorder, CNS disorder, stroke; Huntington's disease; movement disorder; dyskinesis; atchein disorder; movement disorder; degenerative disorder; Parkinson's disease; Alzheimer's disease; ataxia; supranuclear palsy; metabolic disorder; cardiovascular disorder; anorexa; proliferative disease; psoriasis; hyperproliferative disorder; hormonal disorder; polycystic ovarian syndrome; alopecia.

Homo sapiens.

41..63 /label= Transmembrane domain 1 76..98 /label= Transmembrane_domain_2 Transmembrane domain 3 Transmembrane_domain_5 'label = Transmembrane_domain_b 'label= Transmembrane domain 7 Transmembrane domain 4 Location/Qualifiers /label= Tr 170 .307 117..139 label= label= Domain Domain Domain Domain Domain Domain Domain

W0200177175-A2.

18-0CT-2001

U6-APR-2001; 2001WC-US11331.

05-DEC-2000; 2000US-251313P.

(PHAA) PHARMACIA & UPJOHN CO

Sejlitz T, Berthold M; Vogeli G, Lind P,

2002 017449/02.

N-PSDB; AAS16253.

Polynucleotide encoding novel G protein-coupled receptor-2037 and polypeptide useful for identifying modulators useful for treating disorders such as autoimmune disorders, stroke, diabetes, cancer, alopecia, anorexia

Claim 31; Page 61; 101pp; English.

protein-2037. The polypeptide (II) is useful: as a vaccine in a mammal against (11); for identifying a compound binding to (II) preferably compounds useful for treating mental disorders; for identifying a compound modulating activity preferably neuropeptide binding or signalling of (II) and for purifying a G protein from a sample containing to G protein. The polyprucleotide (I) is useful for identifying a compound which binds to (I) encoding (II) and for identifying an animal homologue of (II). The method comprises DNA hybridisation or computer homologues to identify nursels cash sequences of the animal that are homologus to (I). The compounds identified by the screening methods are useful for treating disorders which include thyroid disorders, renal The invention describes the novel isolated G-protein coupled receptor

Ċ tailure, inflammatory conditions e.g. Crohn's disease, diseases related to cell differentiation and homeostasis, rheumatoid arthritis, autoimmune disorders, movement disorders, CNS disorders e.g. stroke, dyskinesias such as Huntingron's disease or Tourette's Syndrome, attention disorders, and degenerative disorders such as Parkinson's, Alzheimer's, movement disorders, including ataxias, supranuclast palsy, infections, caused by human immunodeficiency virus (HIV), or HIV-2, metabolic and cardiovascular diseases and disorders e.g. type 2 diabetes, anorexia, proliferative diseases and cancers, and hyperproliferative diseases and cancers and diseases and cancers and diseases and diseases and diseases and diseases and diseases and disea 0.40 600 C 0 € 101 REGLYGUWYWMITYKYPTVSESQETPAGNSEGLPPKVPSPESPASIPEKEKPSSPSSGKG 160 61 HSLILNLSLADLSLILFSAPIRATAYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVA 129 080 103 314 REGIKGVWKWMTTKKFFTVSESQETFAGNSEGLPDKVPSPESPASIPEKEKPSSFSSGKG +73 Gaps 1 MNVSFAHLHFAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAWFGKPSM1 60 74 HSLILNLSLADISLILPSAFIRATAYSFSVWDLGWPVCKSSVWFIHTCMAAFSITIVATA 121 KVCFMYASDPAKQVSIHNYTIWSVLVAIWTVASLLPLPEBEWFFSTIRHHEGVEMCLVDVPA 134 KVCFMYASDPAKQVSIHNYTIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPA 194 VAEEFMSMFSKLYFLLAFGLELFFASFYFWFAYPQCYKFSTRYCNIFYSVTFFVTANTA 241 SIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEF 254 SIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFIVMSEEF 14 MNVSFARLHFAAGYLPSBEGDWPTIFALLVAVGLVGFVGRLGVISILLHYAWKGFRSMI 181 VABERMSKESKLYPILARGLPLEPASFYFWBAVIGCKKESTKIGNLFNGTRGEGVTVVT 100.0%; Score 2167; DB 23; Length 419; 100.0%; Pred. No. 2.6e-191; tive 0; Mismatches 0; Indels 0; 374 KTEKARIPILPEDVEOFFWHERDTVPSVQNNDPIPWEHEDQETGEGVK 419 361 KTEKAEIPILPDVRQFWHEPDTVPSVQDNDPIPWEHEDQETGEGVK 406 Pred. No. 2.6; Mismatches 406; Conservative method of the invention. Best Local Similarity 419 AA; Sequence Query Match Matches qq ò ם qq S g ç ò

AAE17082 standard; Protein; 419 AA AAE17082

AAE17082;

(first entry) 18-APR-2002

Human G-protein coupled receptor (GPCRx20) protein.

Human, G-protein coupled receptor, GPCPx20, rerehreprotective, vomiting, receptor-mediated disorder, thorapy, urinary retention, allergy, observing seteoporosis, anglaria, establish, and an appetential restances and theresion, anorexia, tumorum migraine, acute heart failure, ulcer, antinuflammatory, stroke, hypertension, neuronal disorder, myotaxidal infarting psycholog depression, mental retardation, neurodegenerative disease, antibuscies, Alzheimer's disease, dementia, ischaemia, Parkinson's disease, antiviral, Huntington's disease, anxiety, antifungal, immunosuppressive, cynoration, vulnerary, analgosic, anorecties, cancer, tranquillizer, neuroleptic, antiemetic, vasorropic, diabetes, cancer, tranquillizer, neuroleptic.

Homo sapiens.

Key

Location/Qualifiers

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196.0%, Pred No. 2 Aerigi, ...
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11.JUL 2600, 2000US-217494P.
26-JAN-2001, 2001EP-0870015.
12-FEB-2001, 4001EF 0870024.
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The present sequence represents a human G protein to refer the protein in the transfer of referred from Indonesia and the referred from the diseases including Mypertension, autoimmune diseases, hear faither meningitis, atopic dermatitis, pneumonia, Alzherents from the companion of thoses. Only a disease, which we disease, the defendance of the companion of the 
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Human; G protein-coupled receptor, GPCE, GAL4, galanin receptor;
Alzheimer's disease; amyotrophic lateral sclerosis; atthma;
atheresclerosis, basal cell carsinoma, breast carchina, carlinguath;
chondrosarcoma; chronic obstructive pulmonary disease; Cichi & disease;
depression; epilepsy; macular degeneration; lymphoma; melanoma;
multiple sclerosis; osteoarthrifts; osteoprosis; parkingon's disease;
psoriasis; rheumatoid arthrifts; osteoprosis; parkingon's disease;
psoriasis; rheumatoid arthrifts; schizophrenia; ulcerative colitis;
hormonal release disorder; cardiovascular activity disorder;
pain perception disorder; cardiovascular activity disorder;
diabetes; hyperlipidaemia; stroke; gene therapy.
                                     GPRV12, GPRV1A
      The invention relates to nine human guanosine triphosphate binding protein (5 protein) coupled receptors designated GPBv12, GPBv11, GPBv12, GPBv11, GPBv11, GPBv11, GPBv12, GPBv12, GPBv12, GPBv12, GPBv11, GPBv11, GPBv11, GPBv12, and to the genes encoding them. These genes and proteins and antibodies against the protein are useful in the treatment, prevention, diagnosis and investigation of diseases associated with G protein-coupled receptors, including cancer, cirrhosps of the liver and Alzheimer's disease. The prosent sequence is a G protein coupled receptor of the invention.
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Best Local Similarity
Matches 405; Conserv
                                                                                                                                                                                                                                                                          Sequence 419 AA;
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                                     Gaps
                                                                                             1 MNVSFAHLHFAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGKPSMI 60
                                                                                                                                                     14 MNVSFAHLHFAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNI,CVIGILI,HNAWKGKPSMI 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 VAFEFMSMFGRIYPILAFGLPLFPASFYFWPAYDQGRRPGFPQNLFNQIRSPQVTVMLL
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         Pred No 4 8e-191;
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99 A%; Pred ...
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31-MAR-2000; 2000JP-0101339.
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         Best Local Similarity 99 RM
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The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCP sequences (including antisense probes), a host cell comprising an expression vector comprising the GPCP sequence, antibodies raised against the polypeptides, and methods of identifying modulators of the polypeptides. The polypeptides are useful for identifying modulator compounds which function as modulators, activators, repressors, agonists or antagonists of the novel GPCP polypeptides including the GAL4 polypeptide. The antibodies and nucleic acid probes as described above can be used to determ the presence of the polypeptides and nucleic acid probes as described above can be used to determ the presence of the polypeptides in which GPCPs are involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g., Alzheimer's disease, amyorrophic lateral sclerosis, asthma, atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy, chondrosarroma, chronic obstructive pulmonary disease, Trhhu's disease, depression, epilepsy, marular degeneration, lymphoma, melanoma, multiple sclerosis, osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other diseases listed in the specification. The probes and antibodies are also useful for diagnosing cognition and memory disorders, anorexia, hormonal release disorders, cardiovascular activity disorders, pain perception disorders, obesity, diabetes, Alzheimer's
                                                                                                                                                                                                                                                                               Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR of the invention.
                                                                                                                                                       Fabre-Suver C, Pritchard D;
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 122, 144pp, English.
                                                                                                (LIFE-) LIFESPAN BIRSTIFWTES INC
                                                                                                                                                       Miller M, Burmer G,
                   11-MAY-2000; 2000US-203217P.
18-MAY-2000; 7000US-205945P
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99.8%; Score 2162, DB 23, Length 418, 100 0%; Pred. No. 7 40-191; tive 0; Mismatches 0; Indels 0
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 28, 2003, 11:48:36; Scarch time 35 Seconds (without alignments) 2390.147 Million cell updates/sec Run on.

....gpNnPIPWEHEDQETGEGVK 406 US-09-828-432-3 2167 1 MPUSPAHLHFAGGYLPSDSC Title: Perfect score. Sequence.

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 seqs, 206047115 residues Searched:

Total number of hits satisfying chosen parameters:

671580

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-plocessing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

1: Sparchea:
2: Sparchea:
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4: Sphuman:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	251	11.6	380	Ŋ	Q9NFV1	Q9nfv1 lymnaea sta
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--- SIMILARITY BELOWS TO FAMILY I OF G-PROTEIN COURSED PECEPTORS EMBL, AJ270461; CAB77264.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Mollusoa, Gastropoda, Pulmonata, Basommatophora,
                  194 VAEPEWSMESHLYPLILAFSLPLFFASFYFWDAYPQCKFGTKTQNLFNQ1FSKQVTVMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 GNLCVIGILLHNAWKGKPSMIHSLILNLSLADLSLLLFSAPIPATAYSKSVWDLGWFVCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ILLOFGVENTVHEGENPSACLNLKELKEPEAGKAFFGSFLFFGYVIPLGVIMLMYGLMLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.6%; Score 251; DB 5; Length 380;
23.2%; Fred. No. 4.2e 12;
tive 68, Mismatches 153; Indels 7
                                                                                                                                                                                                                                                                            374 PTERAFIPII PINUEGPWIEPITVPSVGPNDPIPWEHERGETGF3VK 419
                                                                                                                                                                                                                                                        341 MTEMAFIPILPPVFQPWHERPTVPSVQPNPPIPWEHEPQFTGEGVM 404
                                                                                                                                                                                                                                                                                                                                                                                                                            Q9NFV1;
01-00T 2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-00T-2000 (TrEMPLrel. 11, Last annotation update)
G-profein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                            380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lymnaea stagnalis (Great pond snail).
                                                                                                                                                                                                                                                                                                                                                                                                          FRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  foresers, IFFGGGT9E, GFGE Fh dpgn
Pfam, PFGGGG1; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.29
Matches 89, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lymnaeidae; Lymnaea
NCBL TaxID-6523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; PO2699; 1FAR
                                                                                                                                                                                                                                                                                                                                                                                                        O9NFV1
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104. ATGYALPVWPFGDIGFFWTGYAMYVÄAYASVTTI VIMSLEBYLAVGRALLAMIL BOERRIT 1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AT THE TANK OF THE PROPERTY OF
                                                                                                         293 HAPHTIFHISTMEAANCLAYMNGCWIFILYAFLGENFERGFFERFINTT TFEMFFERFING (*)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 VIVVVIPAICWLPIQIILFARRFOHAPNTIPHISTMSAANCLAYMMSTVNFILMAFU 🖙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Hash mustrib to;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 FTIIPALLVAVOTVOPVOMOVIOTILHMARYOPPORTHOTINES TOGOTTERSKEIN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 ATAYSESVWEEDWEPVESSPWETHTOWARDS STOVARW FRANKESTEARUSTER TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAP LOTALISADINI PENDANINGMEDAA OPALLISEDALISED NELLATION AND THE PARTIES
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PROSITE, PSSAAZAT, G FRONDEN REGER EL 2. 1.
G-protein coupled receptor: Gloroproprofein; Roceptor: Transmontans
SEQUENCE - RELAA, 41540 MM. 1. FEATSPEARITE CREAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.4%; Score 247.5; DB %; Lenth and;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 PRESPREDCTESSPREYERINGPTVICK PITTING CONNECTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68; Mismatches 144; Indels
264 KAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEFREGLKGVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Last sequence update of 1-01N-2002 (TrEMBLrel. 21, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 7.9e 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 WSVIVAIWTVA- -SILFLFEWFFSTIFHHFFTTEWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 KLYFL -- - LAFSLFLFFAGFYFWRAYDQCPFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lymnaca stagnalis (Great pond snail).
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Pfam, Phonobol, Tum 1, 1.
PEINTS, PPONDARY, GEOFFENDORN.
PRINTS, PROISTA, NPEPERCENTOR.
                                                                                                                                                                                                                                312 ----ITKKPPTVSESQETPAGNSE 331
                                                                                                                                                                                                                                                                                                                                                      353 VPFTVTEK-PTTTTTKOTCVNNSK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 22.7%
hes 74, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPELIMINAPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -Coll-Sano (Tremplye)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lymnaeidae, Lymnaea.
NCBL_TaxID=6523,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09NFV2:
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162 ALCEIVIIIIASQIPVG-----PMHGIYVYDFIMBKRSTGAILTIATABATPTMARIY 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIBVVLYGUMLPYLWPMPFPGNSQSVGGPWLTNPDSGSSTPRPP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 ----SKQVTVMLLSIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFI------ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 236; DB 5; Length 444;
; Pred. No. 7.9e-11;
60; Mismatches 127; Indels 68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 AYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVAKVCFMYASDPAKQVSI---HNYTI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 DYAAPTWIFPEWTCSMINFFCHTSAYGSVWTLTTMALDRYLAVVYPVESMTLRTPRNTVI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 WSVLVAIWTVASLLPLPEWFFSTIRHH-----EGVEMCLVDVPAVAEE----- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 EATAARRKUTPLULGULITWALGWLPLNUCFF ----MSGLAYPEPLUISHGUIMVIVQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 IIPTIFAVIILVGLVGNALVVIVAFGROMR----NSTNTLIIGLAISDLMFLLLCVPFTAV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lymnaea stagnalis (Great pond snail).
Eukaryota, Metazoa; Mollusca, Gastropoda, Pulmonata, Bascmmatophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 IIPALLVAVOLVGFVGNICVIGILLHNAWKGKPSMIHSLIINLSLADISLLLFSAPIRAT 84
                                                                                                                                                                 Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
schore 28.12.02.2018 (1988).
SUPCELULAR LICATION: INTESPAL MEMBRANE FFOTEIN (BY SIMILARITY)
-: SIMILARITY. BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PP00001, 7tm 1, 1.
PPOSTTE: PS00237; G PPOTEIN RECEP F1.1; 1.
PPOSTTE: PS00237; G PPOTEIN_PECRP_F1.2; 1
G-profein coupled receptor; G1ycoprofein; Transmembrane.
SEQUENCE 444 AA, 49814 MW, 2CF41F429B302AE2 CRC64;
                                                                                                                                                                                                                                                                             Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                    01-NOV-1996 (TrEMBLrel 01, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 ALSQVLMFSISSANPLIFLVMSEEFREGLKGVWKWMITK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 IASQVLAYTHSCLNPILYALMSQSFREGFIPVMFMLINK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AA.
                    444 AA.
                                                                                                                                                                                       Phabditidae, Peloderinae, Caenorhabditis.
                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
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                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, 266567, CAA91489.1, -. InterPro, IPPnnn9776, GPCP_Phodpsn
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%,
24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 24.8 es 84; Conservative
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                    PRELIMINARY;
                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 FMTFNVF3T7LPL
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                ZY455 3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                      023497;
                                                                                                                                  ZK455.3
                      023497
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023497
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 RIIVPTIFGVICILGLEGNSLVILVVSD--KHMRNTTNILLESLAVABLLFILFCVPFT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 WSVLVAIWTVA----SLLPLPEWFFSTIRHHEGVEMCLVDVPAVAEE-----FMS- MF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 GKLYPL----LAFGLPLFFASFYFWRAYDQCKKR. ...-STFTGALENGLFSKUVTTA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 GYVIPLGVTWLMYGLML------- KPLLYGVVFGGGNGEAESIRAHHBATRM 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 ILSIAIISALLWLPEWVAWLWVWHLKAAGPAPP©GFIALSQVIMFSISSAWFLTFUVASE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 ATAYSKSVWOLGWEVCKSSDWFIHTCMAAKSLTIYVVARTVCFNYASEFARGVSTHN-YTT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 ATGYALPVWPFGDIGCKMTQYAMYVCAYASVYTLVIMSLDRYLAVVHAIRSMTLRSERNT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-1e5
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                                                                      Saunders S.E., Burke J.F., Benjamin P.R.; "Multimeric CREB binding sites in the promoter regions of a family of orphan G-protein coupled receptors related to the vertebrate galanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 RTIIFALLVAVCLVGFVGNLCVIGILLHNAWKGKPSMIHSLILNLSLADLSLLLFSAPIR RL
                                                                                                                             and nocloeptin/orphanin-FQ receptor families ";
Submitted (OCT-1999) to the EMBL/GenBank/DDB4 databases.
-!- SUBCELLULAE LOCATION: INTEGRAL MEMBERNE FROTEIN 18% SIMILARITY
-!- SIMILARITY RELONGS TO FAMILY 1 OF G-FROTEIN CUSTLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                     PPOSITE; PS002'0'; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50.2C; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50.2C; G_PROTEIN_RECEP.F1_2; Transmembiano.
G-protein coupled receptor; Glycoprotein; Receptor; Transmembiano.
SEQUENCE 380 AA, 42723 WW; D54FSEE28BEE4EC4 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 WFAILLIWIIILCGNTFILLQFGVFNYVHEGENRSACL-NLKELKEHEAGKAFFGSFLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sia G.M., Maggio J.E., Too H.P.; "Construction of a functional EGFP-tagged avian substance P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- KWMITKKPPTVSESQETPACNSE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 22 6%; Pred No 1 26-10;
nes 79; Conservative 69; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%, Score 232.5; DB 5
22 6%; Pred No 1 2e-10;
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                                                                                                                                                                                                                                                             IPPONN276; GPCP_Phodpsn
                                                                                                                                                                                                                    EMBL; AJ270462; CAB77265.1; -.
                                                                                                                                                                                                                                                                                               PRINTS; PR00237; GPCPPHODOPSN PRINTS; PR01570; NPFFRECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken)
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                                                                                                                                                                                                                                                                                Pfam; PF00001; 7tm 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 EFREGIKGUW---
Lymnaeidae; Lymnaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
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                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  · · · · · PEWVAWLWVWHILFAAGPAPPQGFIALSQVIMFSISSAMPLIFLVM 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 VNETYAIHNEWYYGLLYCKFHNFFPIAAVFASIYSMTAIALDPYMAIIHPL-OPPLSATA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 [WSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPAVAEEFMSMFGKLY----- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TKVVICVIMILAFILAFPGGYYSVTEELPGFLVCLVAWP---EHSTRVYGKTYHPCMTVL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 TO THE APPERENCE FRANK AVERTHEN THE SERVENT SERVENT STATES AT 1948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF131057, AAD3107.1; --
HSSP, P29274; 1MMH.
InterPro, IPPAnon76; 1CPTP Phodpsn.
PFANY: PROACH; 7CPTP Phodpsn.
PRINTS; PROACH; 7CPTP PROACH; PRINTS; PRO1565; NBUROMEDIUR;
PRINTS; PRO1565; NBUROMEDIUR;
PRINTS; PRO1565; NBUROMEDIUR;
PRINTS; PRO1565; 1CPTEIN RECEP F1.1; 1.
PPANY: 1S4. 27.3; 1CPTEIN RECEP F1.1; 1.
G-protein coupled; 1CPTEIN RECEP F1.1; 1.
G-protein coupled; 1CPTEIN RECEP F1.1; 1.
G-protein coupled; 1CPTEIN RECEP F1.2; 1.
PROFERENTER F1.3; 1CPTEIN RECEP F1.3; 1.
PROTEIN RECEP F1.3; 1CPTEIN RECEP F1.3; 1.
PROTEIN RECEP F1.3; 1.
P
- - SIMILAPITY - BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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Bukaryota, Metaroa, Chordata, Craniata, Vestebrata, Euroloostomi,
Mamonilis, Estlosia, Rodenia, Hystricoguathi, Cavidae, Cavia.
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Best Local Similarity 24 1%; Prod No 26-10;
Matches 92, Conservative 53; Nismatches 142, Indels 57,
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Studm R.F., Perst C., Schaefer M.K.H., Weihe E.;
"Cloring And Sequenting of guine; Fig 3R3 reletor",
Submitted (APR-2000) to the EMBL/CenRank/DDRJ databases.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAP-2002 (TrEMBLrel 70, last annotation update)
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Inti-Pro; IPPOA6274; GPCP Phodiss
Pfam; PF00001, 7tm 1, 11

PROSITE, PS00267; GPROTEIN PROFF F11; THENOW: 1

PPOSITE, PS50262; G_PROTEIN PROFF F12; 11
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22 WFTIIFALLV AVGLVGFVGNLCVIGILLHNAWKGKPSMIHSLILNLSLADLSLLFSAP 80

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81 IPATAYSKSVWPLGWPVPESGWFIHTCMAARFOLFIVWAARVCHWYLSGGAR 1807 189
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J. Nauthernia 21.0027 935(2001).

EMBLY ANGSBOTI, AARS9999 1;

InterPro: IPR00276; GPCF_Rhodpsn.
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01-MAR-2002 (TrEMBLral 20, Last sequence update)
01-JUN-2002 (TrEMBLral. 21, Last annotation update)
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Ill SRUIBNCE FROM N.A.
Saunders S.E., Birke J.F., Renjamin P.R.;
Saunders S.E., Birke J.F., Renjamin P.R.;
"Multimeric CREB binding sites in the promoter regions of a family of orphan G-protein coupled receptors related to the vertebrate galanin and nociceptin/orphanin-FO receptor families.";
Submitted (ACT-1999) to the EMBL/GenBank/DDBJ databases.

PMRE: AJ270459, CAP77262.1;
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                                                                                                                                                                                                                            PRELISPVESERVAWTERSHOPRALLANHHELPSSOIQSGRIDESSV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEAM; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01577; NPFPROFERPOR.

PROSTE, FS50263; G_PROTEIN_RECEP_F1_2; 1.

G_PYOLEIN COUP.64 receptor; Receptor.

SEQUENCE 386 AA, 42773 MW, DPRIESEA20072629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUM-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lymnaea stagnalis (Great pond snail).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-protein coupled receptor.
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Best Local Similarity
For 78; Conserva
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P. C. Digit anniana familia.

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181 -VAEEFMS--MEGKLYPLLAFGLELFASFYFWHATDO EFFSTFILMIEL FL. 18. F.
                                                           146 SRMMRTENITLIAI VTIMIVVIJVIJVIRINY
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es 78; Conservative
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                                                                                                                                                                                                                                                                                                          292 IPLUMSEEFFE 302
                                                                                                                                                                                                                                                                                                                                                  310 LYRELDENFER 322
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                                                             Eukaryuta, Metaloa, Arthripuda, Tishbara, Bronyoda, Tushma,
Prerygota, Mesttera, Endopterygota, Diptera, Brachyoera, Muscomerpha,
Ephydroidea, Drosophilidae, Drosophila.
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132, indels 44, Gaps
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PROSITE, ESCOSS, G-FACILIN RECEFFI. 1.
PROSITE, PSSOSS, G-PROTEIN RECEFFI. 2. 1.
C-protein coupled reseptor. Navogrant etc. Transmembitate
sequence 339 AA, 37520 MW, 7512P74F8944DBA FPG64.
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20.18; itel E. 188 ...
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InterPro, IPR002106; AALRNA ligaseII.
InterPro, IPR000276; GFCR_Rhodpsn.
                             AR-2 0K (G19001.
Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                      SEQUENCE FROM N.A.
      CG10001 protein.
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181 VABBEMS MEGRUFICIANFERENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTERMENTE
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196 FINSELSTRUCTFICOTIONSTANDSTANDSTANDSTANDS TO NEW FILLS SEED
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allatostatin receptor from Diorophila molanovario: ";
Biochem. Biophys. Res. Commun. 273:571-577 (2007).
FMRU, APS-1265, AAF-1261.1;
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Communication of the Score 2013; Pred No. 1.76 09; See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Mismatches 152; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; Jubeln See 57; 
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AP.2 OF 0310001.
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Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                        Lundell I., Boswell T., Larhammar D.,
"Chicken Neuropeptide Y Family Receptor Y4; a Peceptor with Equal
Affinity for Pancreatic Polypeptide, Neuropeptide Y and Peptide YY.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
FMRI, AF410RE3, AAL8416; 1;
                                                                                                                                                                                                                                                                          Eukaryofa, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 WEVCESSEWFIHTCMAARSLTIVVVARVCEMYASDPARQVSIHNYTIWSVLVA----- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFHQ1 IINPTGWPPSISQAYLGIG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 PILAPGLPLFFASFYFWRAYDQCKKPG···TKTQNLRNQIRSKQVTVMLLSIAIISALLW 250
194 FTTNDFLOPPTYQVTFFISSYLAPLMIISGLYMRMIMPLWPQGTGVRMSKESQRGRKRVT 255
                                                   256 RLVVVVVIAFÄSLWLPVQLILL....LKSLDVIETNTLTKLVIQVTAQTLAYSSSCINFL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 VLGIVGNICLIAVIAPO PEFTNVTNILISNLIISPLFMCLVCLPFTVVYTMMDYWIPG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 LLLQYCIPLFFILLCYLPIYLPLQKRKPMFEKSEYSNPAVÇLPRINILLASMVAAFAVCW 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; GADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 LUGFUGNICUTGILLHNAWEGEFSMIHSLILNESLABLSLLLFSAPIRATAYSKSUMBLG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Arthropoda, Tracheata, Hoxapoda, Insecta,
Prenygora, Neoprera, Endoprerygria, Lepidoprera, Glossata, Ditrysia,
Bombyocidaa, R.m.bycidae, Bomkyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 LPEWVAWLWV-WHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEFREGLKGV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 LPLHVENTIVDWNYKIISPCHHNLIFSLCHLVAMASTCVNPVIYGFLNSNFKKEVKSL 335
                        237 VMLLSIAIISALLWLPEWVAWLWVWHLKAAGPAPFQGFIAL-----SQVLMFSISSANFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.0%; Score 217.5; DB 13; Length 22.8%; Fred. No. 1.9e-69; ive 66; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             377 AA, 42372 MW, C9RCECOODEFD1F3E CPC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN 2002 (TrEMBLrel. 21, Last annotation update)
Allatostatin receptor RAP
                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel 21, Last sequence update)
01-JUN-2002 (TrEMBLrel 21, Last annotation update)
                                                                                                                                                                              277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 EVMCPMTSFTQCTSVTVSILSLVLIAL
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                                                                                                                                                                              PPT;
                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel 71 Neuropephide Y receptor 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPELIMINAFY,
                                                                                                                                                                              PRELIMINAPY;
                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rombyx mori (Silk morh)
                                                                               292 IFLUMSEEFEE 302
                                                                                                        312 LYAFLSENFRK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Q8QGM3
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SEQUENCE FROM N A
STATIS-LEVON 200 BAB,

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STATIS-LEVON 200 BALLYON 300 AB;

XX SACHELT T. Len;

XX HELLINE-21601656; FubMed=11590150;

XX SACHET T. Len;

XX Hansen G.N., State P., Grimmell-Khuijren C.J.P.;

XX Hansen G.N., State P., Grimmell-Khuijren C.J.P.;

XX Hansen G.N., State P., Grimmell-Khuijren G.J.P.;

XX HALST Cloning of a Functional Allatostatin Gut/Brain Receptor and T. Molecular Cloning of a Functional Allatostatin Gut/Brain Receptor T. J. Riol. Chem. 274-47065-47060[2001]

XX HALST Cloning Of a Functional Allatostatin Gut/Brain Receptor DR BMBL; AF303369; AAL47056-1; JOINED.

EMBL; AF303369; AAL47056-1; JOINED.

EMBL; AF303369; AAL47056-1; JOINED.

EMBL; AF30370; AAL47056-1; JOINED.

EMBL; AF30370; AAL47056-1; JOINED.

EMBL; AF30370; AAPHANA ligasell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEALMFYHITYFTVTAQIVCHVLAYMMSCUMPVLYAFL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 VVPIEFGFIGIVGLVGNALVVLVVAAN POMRSTINLLIINLAVÄMLLEVIEGVEETAT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 AYSESVWELTWEVÇESEWETHTOMAARSIJIVVVAEVÇEMYAGITAFÇVETERYTIMOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 LVA---IWTVASLLPLP-----EWPFSTIRHHEGVEMCLVDVPAVAEEFMSMFGKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 LLÁIACIWVVILTTAIÞVGICHGERÈYSYFNRNHSSCV--------FLEEFG-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 PILAPGLPIFFASF ---- YFWBAYDQCYYBGTYTQNLBNGIRCHQYMNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 SKLGPQMSFFLSSYVIPLALISVLYWOMITPIWFSAFGGPVSAESPFGF. PPMTRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Euthoria, Podentia, Sciurgmathi, Murihae, Virinae, Mon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 68; Pred No cross.
tive 52; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 AA, 40478 WW, 63C2B2846FC3010A CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01 MAP.2002 (TrEMBLrel. 20, Last annotation update)
SomatoStatin subtype 5 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PRO001, 7Em 1, 1.

PRINTS, PRO0237, GFCRRHODDEN.
PROSITE, PRO0337, AA TPNA LIGASE II 2, THENOWN 1.
PROSITE, FSOC337, 3 FPOTEIN RECEF FI 1, THENOWN 1.
PROSITE, FSOC322, GFROTEIN RECEF FI 1, THENOWN 1.
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O'Carroll A -M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 GELSENEPGREP----RAICT PROYNUED-----ADAIEDP PORSOPPOT--TUPTP----S 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ETIIPALLVAVCLYSEVGNICYIGIDIMAWFGMPSMIHSLI 64
                                  InterPro; IPR0002)6; GPCR_Rhodpsn.
Priam; PR00001; 7rm_1; 1.
PROSITE; PR00237; GPCRHUDOFSN.
PROSITE; PS00237; GPPOTEIN_PFCEP_F1_1; 1.
PROSITE; PS00237; GPPOTEIN_PFCEP_F1_2; 1.
G-10.0. Miled: Wargered and Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken Marken M
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Rest Local Vimilarity 14 mt, Prod. No. 3 46-09;
Matches 89; Conservative 67; Mismatches 164; Indels 51;
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HSSP; P02699; 1F88.
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Search completed: January 28, 2003, 11:51:30 Job time : 38 secs

374 CEANGLMCTSR 384

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GenCore version 5.1.3
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OM protein - protein search, using sw model

January 28, 2004, 11-49-21, Search time 21 Seconds (without alignments) 1858.599 Million cell updates/sec Run on:

US-09-828-432-3 2167 1 MNVSFAHIHFAGGYLPSDSQ.....QDNDPIPWEHEDQETGEGVK 406 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched: 283224 Total number of hits satisfying chosen parameters.

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	galarin receptor	galanin receptor	Lucocor	hypothetical prote	neurokinin 1 recep	in	e-4		ď	3 1	glucocorticoid-ind	eurokinin 3	ч		probable allatosta	angiotensin II rec	compesin receptor,	C)	C 1	N	angiotensin II rec	н	D)	Ξ		pancreatic polypep	kinin	rot	
	Q H	JC5949	159336		T27866	351	622	343	S20304	A44081	JQ1517	040470	S55524	0.1	A34916	\vdash		7	56	800516	3673	4.	820303	18	A44092	121059	G02300	26	830508	
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Result	NO.	; ; ; ; ;	(1	٣	4	'n	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	ed Cd	C1	23	24	25	56	C1	28	

galanin receptor 1 - human C.Species: Homo saptens (man) C.Date: 31-May-1996 #sequence revision 31-May-1996 #text_change 21-Jul 220^ C.Ancassion: 159334; JrSAn1; G01764; G02528

PESULT 2 I59336

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197.5	6 6 1.0	430 328	C1 C4	I51898 I38973	cholecystokinin A G protein-coupled

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A;Reference number: A40470; MUID:92123228; PMID:1663214
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                                                                                                                                                                      A, Molecule type: mRNA
A, Pesidues: 1-423 < HAP>
                                                           A;Accession: B40470
A;Status: preliminary
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A.Molecule type: mRNA
A.Residue: prediminary, translated from GB/EMBL/DDBJ
A.Residue: page: mRNA
A.Residue: page: mRNA
A.Tible: cloning, physomen 241, 658-564, 1997
A.Tible: cloning, chromosomal location, and transcriptional regulation of the human gala A.Reference number areas, mall sequence number areas, mall sequence number areas, physometric cloning, chromosomal location, and transcriptional regulation of the human gala A.Reference number areas, mall sequence nit shown
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F,Harrigan, M.T., "argement F., Barrywis, 2
Mol. Endocrinol. 5, 1331-1338, 1991
A,Title: Identification of A gene induced by glucoccrticoids in murine T-cells: a potent
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C,Species: Mus musculus (house mouse)
C:Date: 14-Feb-1992 #sequence_revision 14 Feb 1992 #fext_change D0-Apri2000
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F;Habert-Ortoli, F.; Amiranoff, B.; Loquet, I.; Laburthe, M.; Mayaux, J. Proc. Natl. Acad. Sci. U.S.A. 91, 97A0-9783, 1994
A;Title: Molecular cloning of a functional human galanin receptor.
A;Reference number: 159336; MUID:95024044; PMID:7524088
A;Accession: 159336
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A,Map position: 18q23-18q23
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C,Genetics:
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A;Pesidues: 1-423 «HAP»
A;Cross-references: GB:M80481; GB:M80510; NID:q1935010; Fi.N:AAA.2555. Fiis 1417712
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A)Experimental source: clone ZK455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ZK455.3 - Caenorhabditis ologans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #seguence_revision 16 Oct 1999 #roxt Chapte 20 Apr 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 ALSQVIME - - SISSANDI DELVMSEEPER DERVMEWMEDERGETVORSETTALE - R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 ASSHEWANTESENGMEVERFEYEART DEFTURAGETAN TOTTON TENTONETTEN
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Pest Local Similarity 24 %, Prod No. 2.80 ii;
Marches 101, Conservative 60, Mismatches 174, Indels 17.
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24.8%; Pred. No. 3.36-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 24.8%, Frad. No. 3.36-11,
Matches 84; Conservative 60; Mismatches 127;
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A, Peference number 20432
A,Accession: T27866
                                                                                                                                C; Superfamily: neurokinin 1 receptor
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R;Gorbulev, V.; Akhundova, A.; Luzius, H.; Fahrenholz, F.
Biochim. Biophys. Acta 1131, 99-102, 1992
A;Title: Molecular cloning of substance P receptor cDNA from guinea-pig uterus.
A;Reference number. 323510; MUID:92256498; PMID:1374648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Superfamily: neurokinin 1 receptor
C.Superfamily: neurokinin 1 receptor
C.Reywords G protein-coupled receptor; glycoprotein; transmembrane #sratus predicted <TM1>
F.92 55/Domain: transmembrane #status predicted <TM2>
F.117-128/Domain: transmembrane #status predicted <TM3>
F.117-128/Domain: transmembrane #status predicted <TM3>
F.149-169/Domain: transmembrane #status predicted <TM5>
F.250-280/Domain: transmembrane #status predicted <TM5>
F.250-280/Domain: transmembrane #status predicted <TM5>
F.289-308/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurovinin l receptor - guinea pig
N.Alternate names: NK-1 receptor; substance P receptor
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 19-May-2000
C;Accession: S23510; S19198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 IYFLPLLVIGYAYTVVGITLWAS----EIPGDSSDRYHEOVSAKRKVVKMMIVVVCTFAI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 LWLPEWVAWLWVW-----HLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEBFREG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 CWLPFHIFFILPYINPDLYLK --- KFIQOVYLAIMWLAM-SSTMYNPIIYCCLNDRFPLG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...----WMITKKPPTVSESQETPAGNSEGLPDK 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 ----PLLAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLLSIAIIS-AL 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 IPATAYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVAKVCFMYASDPAKQVSIHNYT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80; Mismatches 159; Indels 64; Gaps
                                                                                                                                                                                                                                                       ·-SKQVTVMLLSIAIISALLWLPEWVAWLWVWHLKAAGFAPPQGFI-------275
                                                                                                                                                                                                                                                                                                                     27? EATAAKPYÜTPLVLÇVLİTWALCÜLPLNVCFF-----MSGLAYPEPLVISHGVIMVIVQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 WRTIIPALLVAVTLV-GFVGNLTVIGIII.HNAWKGKPSMIHSLILNLSLADLSLLLFSAP 80
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--EGVEMCLVDVPAVAEE----- 184
                                                                                                                           FM--SMFGKLYPLLAFGLPLFFASFYFWRAYDOCKKRGTKT---QNLRNQ----IR--- 231
                                                                                                                                                                                         215 PMTFNVFGYVLPL---GISVVLYGLMLRKLWDMPRPGNSQSVGGRNLTNRDSGSSIRRRP 271
                                                             162 ALCFIYIIIIASQIPVG-----RMHGIYVYDFIMBKRSTCAILTIATAEATPTWARTY 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL:X64323; NID:g49565; PIDN:CAA45608.1; PID:g49566
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                                                                                                                                                                                                                                                                                                                                                                                             276 ALSQVLMFSISSANPLIFLVMSEEFREGLKGVWKWMITK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 IASQVLAYTHSCLNPILYALMSQSPPEGFIPVMKMLINK 364
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             142 WSVLVAIWTVASLLPLPEWFFSTIRHH--
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A; Residues: 1-407 <GOP>
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Files 316/Domain: transmembrane (Asn) (covalent) #Status profile transmembrane (Asn) (covalent) #Status Files 19716-19716 (Asn) (covalent) (by profein kinase C) #status Files.
Files, 317, 312/Briding site: phosphare (Ser) (covalent) (by cAMP-dependent kinase) #status predict Files, 251, 317, Briding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict files, as a profile (Thr) (covalent) (by profein kinase ("#status predicted") (By profein kinase ("#status predicted")
                                                                                                                                                                                                                                                              somatostatin receptor 3 - human ("Species: Homo sapiens "man") ("Species: Homo sapiens "man") ("Species: Homo sapiens "man") ("Species: Homo sapiens "Figure") ("Figure") ("Figu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays prefer
A,Reference number, 332501, MUID:93238970, PMID:8097479
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A, Introns: #status absent rodopsin
A, Introns: #status absent rodopsin
C, Superfamily: Vertebrate rhodopsin
C, Superfamily: Vertebrate rhodopsin
C, Keywords: G protein. Coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TML>
F, 44-70/Domain: transmembrane #status predicted <TML>
F, 118-139/Domain: transmembrane #status predicted <TML>
F, 115-131/Domain: transmembrane #status predicted <TML>
F, 125-131/Domain: transmembrane #status predicted <TML>
F, 125-131/Domain: transmembrane #status predicted <TMC>
F, 282/Domain: transmembrane #status predicted <TMC>
F, 282/Domain: transmembrane #status predicted <TMC>
F, 283-316/Domain: transmembrane #status predicted <TM
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A;Note: Sequence extracted from NCBI backbone (NCBIN:123685, NCBIP:123690)
R;Corness, J.D.; Demchyshyn, L.L.; Seeman, P.; Van Tol, H.H.M.; Srikant, C.F.; Kent, G.
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372 GPK-ATPSSLELTSNGSSRSNSKTVTESS 399
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A; Molecule type: DNA
A; Residues: 1-418 < COR>
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A/Status: preliminary
A/Molecule type: mRNA
A/Cross.references: GB.XC2024; NID.354206, FIPH.CAA44007.1; FILE-14.")
A/Cross.references: GB.XC2024; NID.354206, FIPH.CAA44007.1; FILE-14.")
B/Crock. G.A.; Elliott, D.; Merwali, A.; Blum, A.M.; Sanit, X.; Tyn.3, E.; Weinster, C.; Tyn.3, 1994
M. Immunol. 152, 1830-1835, 1994
A. Fittle. Molecular avidence that granulema T lymphacytes in Fibilia, in instrument in include the A. Peference number: 156216; MUID-94165478; FMID-812039.
A. Fittle. Molecular preliminary
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A. Status. Freliminary
A. Molecular type: mRNA
A. Cross-references: GB. L27826; NID-9450286; FIDN:AAA17401;; FILE-14-074
Nalternate names: NK-1 receptor, substance P receptor
(Species: Mus musculus (house mouse)
(Species: Mus musculus (house mouse)
(Species: Mus musculus (house mouse)
(Species: 22-Nov 1993 #sequence revision 10 Nov 1995 #text change C. Adminior (Species)
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C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27 Jun 1994 #pext charace - Apt asset
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 WRTIIPALLVAYCLY-GEYGNLCYIGILLINAARGKPEMINGI IINTELALISTILLETAN BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABREMETVTHITTHE ABOUT A TAKAN FULL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 ----PLLAPGLPLPFASFYFWRAYDQCKKRATKTQNLPNGIFSFQVTVM1.31A113 AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIPGEGCERYPEQUEARPRUPAMITHEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 IWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDUPATABETACMFTRLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.5%; Score 227; DB 2; No
Bost Local Similarity 22.6%; Pred. No. 1 56-10;
Matches 88; Conservative 72; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: proliminary, translated from GP/EMPL/DDPA,
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 VPSPESPASIPEKEKPSSPSSGKGKTEKA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 GPK-ATPSSLDLTSNGSSPSNSKTMTESS 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Accession: A44081
R, Xie, G.X.; Miyajima, A.; Goldstein, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Residues: 63.290 /2002>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 GWEPRIVETLEYINPELYLK -- FFIGGYYLA GWALAMSSIWYRPIIYGGLMDRFRLG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL IPATAYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVAKVCFMYASDPAKQVSIHNYT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 IYFLPLDVIGYAYTVVGITLWAS----EIPGDSSDRYHEGVSAMRKVVMMMIVVVCTPÄL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 IMIPEWVAWLWVW-----HLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEFREG 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                  ----RVLLRPSRRVRSQEPTVGP----PEKTEEDB----BEEDGEESREGGKGK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 407,
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22.9%, Fred, No. 1.5e.10;
tive 71; Mismatches 165; Indels
                                                                                                                                                                                                                                       neurokinin 1 receptor - rat
N,Altornate names NY 1 receptor, substance F receptor
C,Species: Pattus norveginus (Norway rat)
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A,Cross-references: GB:M80160
C,Superfamily: neurokinin 1 receptor
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hes 78; Conserva
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A;Residues: 1+443 <HAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Buell, G.; Schulz, M.F.; Arkinstall, S.J.; Maury, K.; Missotten, M.; Adami, N.; Talabd FBBs Lett. 299, 90-95, 1992
A;Title: Molecular characterisation, expression and localisation of human neurokinin-3 r A;Reference number: S20435; MUID:92183914; PMID:1312036
A;Accession: S20435
Pro- Ratl Arad Sci V S A 99, 4124-4128, 1997
A;Title: Expression cloning of cDNA encoding a seven-helix receptor from human placenta
A;Eeference number: A44081; MUTD:9233319; PMID:1315951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NiAlternate names: neuromedin K receptor; NK-3 receptor
C;Species: Homo sapiens (man)
C;Date: 20.Apr.2000 #equence revision 20.Apr.2000 #text_change 19-May-2000
C;Accession. JQ1517; S20435; Z31237
R;Huang, R.R.C., Cheung, A.H., Maxima, K.E.; Strader, C.D.; Fong, T.M.
B;Ochem. B;Ophys. Res. Commun. 184, 966-972, 1992
A;Title: cDNA sequence and heterologous expression of the human neurokinin-3 receptor.
A;Reference number. JQ1517, MUID:92246993; PM:N:N:1374246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWLWVWHIFFAAGPAPPQGPIALSQVLMFSISSANPLIFLVMSBEFRBGLKGVW 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 VACLIPIPEWFFSTIPHHEGVEMCLVDVPAVABEFMS------MFGKLYPLLAFGLPLFF 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 LAPLIAPPOLIYSKIFVAMPGPTLOVVQWPERSPOHPTYHMIVIVLVYCPPLLIMGITYTI 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 VGITLWGGEIPGDIGDK -- - YQEQLKAKPKVVKWMIİVVVTFAICWLPYHİVFILT 297
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A)Residues: 1-465 cHUA>
A)Cross-reference: GR M83471; NID G189223, FIRM:AAAR6366 1; PID:G189224
A)Experimental source: brain
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A; Residues: 1-2, 1', 4-62,'R', 64-465 <BUE>
A; Residues: 1-2, 1', 4-62,'R', 1D, 9246908; FIDN:AAB21706.1; PID:9246909
A; Cross-references: G8302; NID, 9246908; FIDN:AAB21706.1; PID:9246909
R; Takahashi, K.; Tanaka, A.; Hara, M.; Nakanishi, S.
Eur. J. Bicchem; 264, 1025-1033, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                32 AVCLVGFVGNLCVIGILLHNAWKGKPSMIHSLILNLSLADLSLLLFSAPIRATAYSKSVW 91
                                                                                                                                                                                        A, Residues. 1.440 «XIE»
Ajürces-references. GM MA4665, NID.9189391, PIDN.AAA36395.1; PID.9189392
C, Superfamily: neurokinin 1 receptor
C, Keywords. G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                       DB 2; Length 440;
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 24.5%; Pred. No. 2.7e-10;
Matches 74; Conservative 59; Mismatches 124; Indels
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Juccoorticoid-induced receptor, long form PP105 - mouse cyspecies: Mus musculus (house mouse) cyspecies: Mus musculus (house mouse) cyspecies: 14-Feb-1992 #sequence_revision i4-Feb-1992 #text_diation 20 Apr. 2000 CyAccession: D40470 CyAccession: D40470 Mol. Sequence_revision: S. Bourgeois, S. Mol. Endocrinol. 5. 1331-1338, 1991 Apritle: Identification of a gene induced by glucocorticoids in murine T cells: a potential Apritle: Identification of a gene induced by glucocorticoids in murine T cells: a potential Apritle: Identification of a gene induced by glucocorticoids in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potential aprit in murine T cells: a potenti
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A/Gener: GDB:9599126
A/Gross-references: GDB:9599126
C,Superfamily: neurokinin 1 receptor
C,Superfamily: neurokinin 1 receptor
C,Superfamily: neurokinin 1 receptor
C,Superfamily: neurokinin 1 receptor
C,Superfamily: neurokinin 1 receptor
C,Superfamily: ransmembrane #status predicted <TM1>
F,83-111/Donain: transmembrane #status predicted <TM2>
F,102-1147/Domain: transmembrane #status predicted <TM3>
F,102-11/Domain: transmembrane #status predicted <TM5>
F,303-35/Domain: transmembrane #status predicted <TM6>
F,303-35/Domain: transmembrane #status predicted <TM6>
F,333-35/Domain: transmembrane #status predicted <TM6>
F,333-35/Domain: transmembrane #status predicted <TM7>
F,23, 50,73/Binding site: carbohydrate (Asn) (covalent) #status predicted)
                                                                                                                                    one of
A/Residues: 1-438,'F',440-465 <TAK>
A/CLOSS-references. GE.XUS172, NIB.375022, FIDH.CAA4C291.1; PID:aR25638
C/Comment: The endogenous ligand of this receptor is neurokinin 3 (neuromodin K),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 AEBEMS-----MEGKLYPLAFGLPLFFAGFYPWBAY - (TETFFFGTETGMLEGGIRG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 PLVNLAFSDASMAAENTLVNFITALHSEWIFGANTGREGRITAVERSITISMIALAVE 182
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Matches 101; Conservative 61; Mismatches 174;
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Oy 235 VTVMLKSTAITS-ALDMLPEWY.	A) Residues: 1728, 36, 329-332, 334-407 cuers. A) Cross-references: GB:MA6675; NID:0180231 A) Octos in the authors' translation 333 GB; Brown Pet 100 100 100 100 100 100 100 100 100 10		Apricas references: GPP-120007, OMIM:162324 A)Map position: 2pter-2gter C,Superfamily: north-transform receptor C,Superfamily: north-transform receptor C,Superfamily: north-transform from first of TMC E,20 Cq/Domain: transform-transform from predicted TMC F,10 120 Moreain: transform-tr
Db 107 TOMAAKSITIVVVAKVOFMYARDINITLINIFFILDREVUSTWVFSEGMINSBEAGY 152 Oy 107 TOMAAKSITIVVVAKVOFMYARDPAKQVSIHNYTIMSVL	Qy 361 FTERABL-PIL 379 Qy 361 FTERABL-PIL 379	As Residues: 1-385 - MARS. As Residues: 1-385 - MARS. As Cross - references: EMBL.X87823, NID-g961255, FIDB.CAA61298.1, FID-g961256 ByCook, 3.A., Elliott, D., Metwall, A., Blum, A.M., Sandol, M., Lynch, R., Mcinstock, J. J. Immunol. 152, 1830-1835, 1994 AyTitle. Molecular evidence that grandisma T lymphosytes in murine schiefrs—mines manned AyReference number. 156716, Millp.44166478, PMID-3420-36 AyReference number. 156716, Millp.44166478, PMID-3420-36 AyReference number. 156716, Millp.44166478, PMID-3470-36 AyReference number of the residence	MAICHER BE, CORSERVATIVE FOR MISSACHES 134, Indel GE, CAPP 10, CERSAC AND CORSERVATION OF THE CORSERVATION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 PLLIMGVTYTIVGITLWGGEIPGDTCDK-----YHEQLKAKRKVVKMMIIVVVTFAIC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 WLPEWV------AWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 WLPYHVYFILTAIYQQLNRWKYI-----QQVYLA-SFWLAMSSTWYNPIIYCCLN 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 INFIYGLHSEWYFGANYCRFQNFFPITAVFASIYSMTAIAVDRYMAIIDPLKPRLSATAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 TIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPAVAEBFMS-----MFGKLY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 KI--VIGSIMILAFLAFPQCLYSKIKVMPGRTLCYVQMPEGPKQHFTYHIIVILLVYCF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 24.9%; Pred No. 5.30-10;
Matches 78; Conservative 57; Mismatches 132; Indels 46; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 IRATAYSKSVWDLGWFVCKSSPWFIHTCMAAKSLTIVVVAKVCFWYASDPAK-QVSIHNY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 IMLPEWVAWLWVW-----HLKAAGPAPPQGFIALSQVI.MFSISSANPLIFLVMSEEFREG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 FKHAFRCCPFISAGDYEGLEMKSTRYLQTQGSVYKVSRLETTIS----TVVGAHEEEPED 371
                                                                                                                                                                                                                                                                                                                              147 TYVVICVÍMVLALLLAFPOGYYSTTETMPSRVVCMIEMP---EHPNKIYEKVYHICVTVL 203
                                                                                                                                                                                                                                                                                                                                                                                              194 ----PLUAFGLELFFASFYFWRAYDQCKKPGTKTQNLPNQTPSKQVTVMLLSIALIS-AL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 IYFLPLLVIGYAYTVVGITLWAS----EIPGDSSDRYHEQVSAKRKVVKWMIVVVCTFAI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 CWLPFHIFFLLFYINPDLYLK-- KFIQQVYLAIMWLAM-SSTWYNPITYCCUNDRFRLG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------WMITKKPPTVSESQETPAGNSEGLPDK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 WRTIIPALLVA-VCLVGFVGNLCVIGILIHNAWKGKPSMIHSLILNLSLADLSLLFSAP 80
                                                                                                                               91 IBATAYSKSUWDI GWFUÇKSSDWFIHTCMAAKSLTIVUVAKUCFMYASDPAKQUSIHNYT 140
                                                                                                                                                                                               ыя vistyaviniewiyytepiyepiinpepiaavpasiysmtavappymaiihpL-фррцаата 146
                                                                                                                                                                                                                                                              141 IMSVLVAIWTVASLLPDEWFFSTIRHHEGVEMCLVDVPAVAEEFMSMFGKLY----- 193
22 WRTIIPALLVAVCLV GEVGNLCVIGILLHNAWKGKPSMIHSLILNLSLADLSLLFSAP 80
                                          30 WOIVLWAAAYTVIVVTSVVGNVVVMMIIL--AHKRMRTVTNYFLVNLAFAEASMAAFNTV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Residues: 1.452 - SHI>
A)Cross-references: 38 005181, HIP-9205470, FIDM-AAA41688 1: PID:9204671
C)Superfamily: neurokinin 1 receptor
C)Reywords: 3 profein-coupled receptor: glycoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession, A34016
R;Shigemoto, R.; Yokota, Y.; Tsuchida, K.; Nakanishi, S.
J. Biol. Them 265, K23.424 1990
A,Tille. Cloning and expression of a rat neuromedin K receptor CDNA.
A,Reference number, A34916, MIII: 30110113, PMIP 2153166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurokinin 3 receptor rat
N/Alternate names: neuromedin K receptor; NK-3 receptor
C/Species: Patrus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 VPSPESPASIPEKERPSSPSSGKGKTE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 GPF ATPSSIDLTSNCSSPSDSKTMTE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 LKGVWK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type . mPNA
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348 KRFFAGFKRAFRW 360

RESULT 15

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probable allatustatin receptor.2 fruit [ly (Presophila melanogastex)
probable allatustatin receptor.2 fruit [ly (Presophila melanogastex)
C;Species: Drosophila melanogaster
C;Date, 08 Sep.2000 #seguence_revision > Sep.2011 #ter._hlange 02-Avg DSC2
C;Date, 08 Sep.2000 #seguence_revision > Sep.2011 #ter._hlange 02-Avg DSC2
C;Accession (2073)
B;Chen Eiophys Res Commin. 273, 571 577, 2000
B;Chen Eiophys Res Commin. 273, 571 577, 2000
B;Chen Eiophys Res Commin 2073/9
B;Reference number: 3073/9
B;Reference number: 3073/9
B;Reference number: 3073/9
B;Residues: 1-357 < Alma
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C;Superfamily: endothelin receptor B
C;Keywords: extracellular protein; glycoprotein, neuropeptide; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 FITNDFLGERTVQVPFFISSYLLELMILSGLYMEMMELME 251 30FMJFF7315 SEEEVT 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 RLVVVVIARASIMI, BVQLILLI - - LKSLDVIEINTLIKLVLUVTAQTLATSSACTINFT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 MEVILCIPHTATDYMVYYWPYGREWCRSVQYLÍVVTAFÁSIYTLVĽMSIDRFLAVVHPIR 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 GTLP-----W--IVGFFFGVIALIGFFGNLLVILVVVFN: TREESTTYLMINI AAADL PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 GYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAWRGKPSMIHSLILNISLAD: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.1%; Score 218; DB 2; Length 357;
Best Local Similarity 25.1%; Pred. No. 6 8e-10;
Matches 78; Conservative 57; Mismatches 132; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Map position: right arm of chromosome 3, 98D-E A;Introns: 180/3; 273/3; 326/3
C;Superfamily: endothelin receptor B
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Job Lime : 23 secs
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GenCore version E 1 3
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OM protein - protein search, using sw model

January 28, 2003, 11:43:46 ; Search time 14 Seconds Run on:

(without alignments) 1202.914 Million cell updates/sec

US-09-828-432-3

2167 1 MNVSFAHLHFAGGYLPSDSQ. Perfect score: Sequence:

ODNOP I PWEHEDQETGEGVK

Gapop 10 0 , Gapext 0 5 BLCSUM62 Scoring table:

112892 segs, 41476328 residues Searched.

Total number of hits satisfying chosen parameters:

seg length: 20กกอกกกกก Minimum DB seq length: 0

Maximum Match 100% Listing first 45 summaries Post-processing. Minimum Match ∩\$

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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CI	260 €	12.4	346		GALP PAT	e rattus
٣	569	12.4	348	-	GALR MOUSE	9 mus mus
4	567		372	-1	GALS PAT	ratti
5	265		387	1	GALS_HTMAN	33 homo sa
9	262.5		349	Н	SALP HEMAN	homo
7	261	12.0	370	_	GALT PAT	ratti
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6			368	r-4	SALT_HUMAN	
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14	04	0.	407	-	NKIR RAT	ratti
15	224.5		440	-	NK4F HUMAN	P30098 homo sapien
16	CI	ċ.	46.0	-1	NY38 HIMAN	1.0°.
17	C1	C	460	e-4	NF18 PARIT	cryct
18	0.1	c-	285	-	NK38 MOTISE	31.m SC/m
	221	c:	404	- 1	NK1F_HIMAN	
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31	-		9	Н	AG22_MERUN	merione
32	214	9.6	184	, 1	ω. Ω.Ι	P30549 mus musculu
33	213.5		422	r-1	GP72 CANFA	earis f

EMEL, AFC7275; AAC95468.1, -.
MGD, MGI:1337018; Galr2.
Interbro, IRR006276, GFP_Phodpen
PEm, PP00001; 7tm 1, 1;
PRINTS, PP0001; 7tm 1, 1;
PROSITE, PS00237; G_PROTEIN_RECEP_F1_1, 1.

EMBL; AF042784; AAC36589.1; -.

Decies wow 168088				PROGRETALISE DOPY	P51144 mesocridetu		P30972 home capies	PROBLE SIME ELBOYA		Ognsd home sapien	
NY4R HUMAN	22 PAT	CERTHIMAN	CKP_PAT	SSR3 RAT	NK2R MESAU	CCKP MOTISE	SSR1_HUMAN	SSR1_MOUSE	SSE1_PAT	SAPR_HUMAN	SSR3_MOUSE
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASEALMENTON, TURMES 982222, MAGNICO M., Graziano M.F., Bayne M., MEDLINE 99648962, Turmes 4.3, Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S., Mang S.
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Kolakowski L.F. Jr., OrNeill G.P., Howard A.D., Broussard S.R.,
Sullivan K.A., Peighner S.D., Sawdargo M., Nguyon T., Margman S.L.,
Shlao L.-L., Hreniuk D.L., Tan C.P., Evans J., Abramovitz M.,
Charannett A., Conione N. W.G., Johnson M.P., Tharsan A.,
Khoshkonei H., George S.P., Smith P.G., Orlowd B.F.,
"Molegular characterization and expression of cloned human galdon
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Miss.
NCBI_TaxID=10090;
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J. Neurochem. 71.2239.2251(1998).
                                                      STANDARD;
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GALS_MOUSE
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01.NOV.1997 (Rel. 35, Last sequence update)
01.NOV 1977 (Rel. 40, Last annotation update)
03.01.NOV (Rel. 40, Last annotation update)
03.01.NOV 50.01.NOV 1 (GALPI)
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PPOSITE; PSSO262, G_PROTEIN_RECEP_F1_2, 1.
6-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family 27 EXTRACELLULAR (POTENTIAL).
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VF -> CL (IN PEF 2)
A -> V (IN PEF. 2)
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CYTOPLASMIC (POTENTIAL)
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Matches 92; Conservative
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                                                                                                                                                                                           -1. SUBCELLULAR LOCATION: Integral membrane protocol.
-1. TISSUB SPECIFICITY: SPINAL CORP. SMAL INTEGRIES. FINIAP
-1. TISSUB A CELLS AND SEVERAL PEATH METERS. FACTOCOL.
-1. TISSULMMA CELLS AND SEVERAL PEATH METERS. FACTOCOL.
-1. TIPPCOAMPUS, ANTICOLS, SUPRACTIC NUCLEUS, HTT TRAINANCS, THAILANDE,
-1. ATERAL PARARACHIAL NUCLEUS AND LOCUS COEPHIESS
-1. PTM THREE CYSTEINE RECIPIES ARE POWEN IN THE "TERRING AT CALCUM.
-1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN CONTILIES PETHORS.
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Best Local Similarity 27.1%; Pred. No. 6.36 11;
Matches 88; Conservative 60; Mismatches 130; Indels 47; Agrs
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                                                                                                                                                     ii.
                                                       MEDLINE-96363004, Pubmed-8750821,
Parker E.M., Izzarelli D.G., Nowak H.P., Mahle C.D., Ben L.E.,
Wang J., Goldstein M.E.,
                                                                                                                                                   FUNCTION: RECEPTOR FOR THE HORMONE GALANIN. THE A TIVUITY HERECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITY APPROVADE
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Fram_; Frecort, 7tm_; 1.
PPINNS; PROC0237; GPPHONOBSN.
PPGSITE; PSO0237; G-HOTEIN RECEP_F1_1; 1.
PROSITE; PSO0262; G-PROTEIN RECEP_F1_1; 1.
G-profin Compress Procording Procording Procording Procording Procording Procording Procording Procording Palmitate.
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CYTOPLASMIC (POIENTIAL.
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Brain Pes. Mol. Brain Pes. 24:179-189(1995);
-!- FUNCTION: RECEPTOR FOR THE HORMONE GALANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AFICK --- FIH-
                                           TISSUE=Insulinoma;
                         SEQUENCE FROM N.A.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268
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107
318
                                                                                                                                                                               ACTIVITY.
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                                                                                       Wang J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: THREE CYSTEINE RESIDUES ARE FOUND IN THE C-TERMINUS, AT LEAST ONE OF WHICH MAY RE PAIMITOYLATED (BY SIMILARITY) SELONGS TO FAMILY 1 OF G-PROTEIN COUPLED PROEDFIPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain;
MEDLINE=97415411; PubMed=9271210;
Mang S., He C., Maguire M.T., Glemmons A.L., Furrier R.E., Guzzi M.F.,
Strader C.D., Parker E.M., Bayne M.L.;
"Genomic organization and functional characterization of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genemiss 45.434-508(1997).
-!- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE
                                                                                                                                                                  268 AEF--GAFPLTPASFFFRITAHCLAYSNSSVNPIIYAFLSENFRKAYKQVFKCRV---- 320
155 VGFIWALSIAMASPVAYYQRLFHRDSNQTFCWEHWP-----NQLHKKAYVVCTFVFGYL 208
                                        LPLFFASFYFWFAYDQCFYFGTFTQNLPNQIPSYQVTVMLLSIAIISALLWLPEWVAWLW 259
                                                                                200 LPLLLICPCYARVLAHLHER LFAMSKESEASKERTAQTVLVVVVPGISWLPHHVIHLW 267
                                                                                                                            260 VWHLKAAGPAPPQGFI ALSQVLMFSISSANPLIFLVMSEEFPFGLKGVWKWMITKKPP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98635873, PubMcd-9367674;
Jacoby A.S., Webb 3.C., Liu M.L., Kofler E., Hort Y.J., Fathi Z.,
Bottema C.D.K., Shine J., Iismaa T.P.;
Bottema C.D.K., Shine J., Iismaa T.P.;
"Structural organization of the mouse and human GALRI galanin receptor genes (Galnr and GALNR) and chromosomal localization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Choldata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodenzia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                             PS6479;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Galanin receptor type 1 (GALI-R) (GALRI).
                                                                                                                                                                                                                                                                                                                                                               348 AA.
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InterPro; IPP006274; GPCR_Phodpsn
Edm, PR00001; 7tm 1; PP11775; PP00277; GPPPHGOOESN.
PPOSITE; PSGGG17; GPPPHGOPSN.
                                                                                                                                                                                                                                                                                                                                                               PFT,
                                                                                                                                                                                                                                                321 ---- CNESPHGDAKE-KNRIDIPPS 340
                                                                                                                                                                                                               318 TVCESQETFACHSEGLPLEVPSFES 342
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U90655, AAB87748.1, JOINED.
U90656, AAB87748.1, JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GalR1 galanin receptor.";
FEBS Lett. 411:225 230(1997).
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46 MGVLGNSLVITVLARSK-PGKPRSTTNLFILNLSIADLAYLLFCIFFÇATVYALPTWVLG 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- NKLHKKAYVVCTFVFGYL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 LPLILICECYAKVINHIHKK LKMMSKKSEASYKKTAQTVLVAVAVPSISWLEHHVAHLW 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 AEF.-GAFPLIFASFFFRITAHCLAYSNSSVAPINTAFLSEUFFFAYFAVFVOFFSF 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi.
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 VGFVGNLCVIGILLHNAWKGKP-SMIHSLILNESLADLSLLLFSAPIRATAYSKSVWDLG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 APICK - . . FIH - - - YPPTVSMLVSIPTLAAMSVDPYVAIVHSPPSSSIPVSRNALLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 ---IMTVASLLPLPEWFPSTIRHHEGVE-MCLVDVPAVAEEFMSMFGKLYPL--LAFG--
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                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ... FOTENTIAL. ... ILINKED (GLCNAC. ... FOTENTIAL. ... ILINKED (GLCNAC. ... FOTENTIAL. BY SIMILARITY. ... PALMITATE (BY SIMILARITY. ... FFS2D752BAA19F9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97261892; PubMed=9108306;
Howard A D , Tan C , Shiso L L , Palyha O C , Mokee M.K.,
Weinberg D H , Feighner S D , Cascieri M.A., Smith R.G.,
                                                                                                                                                                                                                                                                                                                                                                                   12.4%, Score 269; DB 1; Length 346
28.3%; Pred, No. 6.8e-11;
tive 54, Mismarches 178; Indels
                Transmembrane, Glycoprotein;
                                          EXTPACELLULAR (POTENTIAL)
                                                                                                                                                                  EXTRACELLULAP (POTENTIAL)
                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                    3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                             7 (POTENTIAL).
CYTOPLASMIC (FOTENTIAL)
N-LINKED (GLCNAC.)
                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-2022 (Rel. 41, Last annotation update)
13-JUL-1991 (GALP.)
15-JUL-1992 (GALP.)
                                                                                         2 (POTENTIAL)
                                                                                                                                                     4 (POTENTIAL)
                                                                                                                                                                                                               6 (POTENTIAL)
PPOSITE; PSS0267, G_PPOTEIN_PECEP_F1_2; 1.
                                                            (POTENTIAL)
                                                                                                                                                                                 5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 VGFÍWALSIAMASPVAYHQRLFHRDSNQTFÓWEGWP
                           Multigene famlly, Lipoprotéin, Palmitate.
DOMAIN 1 34 EXTRACPLIUMA
                                                                                                                                                                                                 CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                        39114 MW;
                protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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192
186
319
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172
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247
268
270
291
348
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                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                        348 AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 TVSESQE 324
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152
173
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning, pharmacological characterization and distribution of a novel
                                                                                                                 Smith K F., Forray C., Walker M W., Jones K A., Tamm J A., Bard J., Branchek T.A., Linemeyer D.L., Gerald C.; Expression cloning of a rat hypothalamic galanin receptor coupled to phosphoinsitide turnsver.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FINCTION RECEPTOR FOR THE HORMONE SALMIN AND FOR GALP. THE ACTIVITY OF THIS PECEPTOR IS MEDIATED BY G PROTEINS THAT ACTIVATE THE PHOSPHOLIPASE C/PROTEIN KINASE C PATHWAY (VIA GO) AND THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SURCELLULAR LOCATION: Integral membrane protein.
SIMITARITY: RELONSS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                     Pathi Z., Cunningham A M., Then L.G., Raftaglino P.B., Ward S.A.,
Nichol K.A., Pine K.A., Wang J., Goldstein M.E., Ilsmaa T.P.,
Zimanyi I.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fathi Z., Cunningham A.M., Iben L.G., Battaglino P.B., Ward S.A.,
Nichol F.A., Pine F.A., Wang J., Goldsrein M.E., Iisman T.P.,
                                                                                                                                                                                                                                TISRIBE-Hyporhalamus;
MEDLINBE-974.8353; PubMod 9281594;
MEDLINBE-974.8353; PubMod 9.281594;
Mang S., Hashemi T., He C., Strader C., Bayne M.,
"Molecular cloning and pharmacological characterization of a new galanin receptor subtype.";
Mcl. Pharmartl 62 177 147(1977)
                 "Molecular cloning and characterization of a new receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; Prucou, aprephonesw.

PRINTS; PRACAT; aprephonesw.

PROSITE; PSACAT; FPETER PETER FIL; 1.

PROSITE; PSACAT; FPETER PETER FIL; 1.

PROSITE; PSACAT APPERENT FETER FILT.
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EXTRACELLHUAR (POTENTIAL)
5 (POTENTIAL).
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Brain Res. Mol. Brain Res. 53:348-348(1998).
--- Pimomion - EFEEPTOP FOR THE HORMONE SALAN
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van der Ploeg L H T , Sullivan F A ;
                                                                                                                                                                                    020 04610 04616(1994)
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EMBL; AF008548; AAR67571 1; -
InterPro; IPP00076; GPCP_Phodpsn.
                                                                                                   MEDLINE-97450996; PubMed-9305929;
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98087378; FubMed.9427505;
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                                                 FEBS Lett. 405:285-290(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U94322; AAB53220.1; -.
EMBL, AF010118, AAC51158 1, .
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                                                                               SPOUTENCE FROM N.A.
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TPANSMEM
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Bloomudist Brr., Beauchamp Mrs., Zhelnin L., Brown S. E.,
Sore-Willse A. P., Stegor P., Cornfleld L.J.,
"Cloning and expression of the human plants reporter lasts.",
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Mammalia, Butheria, Primates, Cafarihini, Hominidae, Homo
                                                                                                                                                                                                                                                                                             12.3%; Score 267; DB-1; Lobath RT;
25.1%; Pred. No. 9.9e-11;
tive (c), Migratoboo 174; India
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                                 EXTPACELLILAD (POTENTIAL
                                                                                          CYTCHIACMIC (DOTENTIAL N-LINKED (GLONAC N-LINKED)
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15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-2002 (Rel. 41, Last annotation update)
3-alamin receptor type 2 (UAL2-P) (UALP2).
GALP2 OP GALNP2.
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      F (POTENTIAL)
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      PPANSMEM
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MEDINE-GOOGGAGO, pubmod-GORGOBA, Ponce K.A., Smith K.E., Borwsky B., Walker M.W., Huang L.-Y., Jones K.A., Smith K.E., Hard J., Branchek T. A., Gerald Co., "Cloning and characterization of the human galants "Mulby receptoring";

Peptides 19:1771-1781(1998)

Bicchem. Biophys. Pes. Commun. 243:474 479(1998)

SEQUENCE FROM N.A.

SEQUENCE FPOW N.A. MEDLINE=98352135; PubMed-9645625; Pathi Z., Pattaglino F.M., Then L.C., Li H., Paker B., Chang D.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INHIBIT ADENYLYL CYCLASF (VIA GI)
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSER ABINDANTLY WITHIN THE CENTRAL
NERVOUS SYSTEM IN BOTH HYPOTHALAMUS AND HIPPOCAMPUS. IN PERIPHERAL
TISSUES, THE STRONGEST EXPRESSION WAS OBSERVED IN HEART, KIDNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                receptors GALR2 and GALR3.";
J. Neut.-them 11,2339-27:1(1304)
--- EUNCTION PEOPPOP FOR THE HOPWONE GALANIN AND FOR GALD, THE
ACTIVITY OF THIS PEOPPOP IS MEDIATED BY 3 PROTEINS THAT ACTIVATE
THE PHOSPHOLIPASE C/PROTEIN KINASE C PATHWAY (VIA GQ) AND THAT
                                                                                                                                                                                                      MEDINE-99948961; PhbMod-9922121;
Kolakowski L F Jr , O'Neill G P , Howard A D , Broussard S P ,
Kolakowski L F Jr , O'Neill G P , Board A D , Broussard S P ,
Shiao L - L , Hreniuk D L L , Tan C P , Evans J , Abramovitz M ,
Charenmonf A , Goulombe B , Mg G , Johnson M P , Thirian A ,
Khoshbouei H , George S P , Smith P G , O'Nowd R P ;
"Molecular characterization and expression of cloned human galanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIVER, AND SMALL INTESTINE.
SIMILAPITY: RELONGS TO FAMILY 1 OF G-PPOTEIN COUPLED RECEPTORS.
McGovern P., Mahle C.D., Journell Dickinson P. B.J., Zimanyi I.A., Molecular characterization, pharmacological properties and "Molecular characterization, pharman SALF2 galanin receptor.", chromosomal limitarization of the human SALF2 galanin receptor.", Rrain Res. Mol. Brain Res. 58:156-169(1998).
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N LINKED (GLCNAC, .,) (FOTENTIAL)
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Propertion
PPOSITE; PSC0237; G-PPOTEIN PECEP F1_1; 1
PPOSITE; PSC0262; G-PPOTEIN PECEP F1_2; 1
G-profein Coupled receptor; Transmembranc; Slycoprotein;
Multidene family.
28 EXTRACELLULAR (POTEMTAL)
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EMBL, AF080686, AAD08671.1; -..
EMBL, AF058762, AAC18118.1; -.
EMBL, AF042782, AAC16587 1; -..
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12.1%; Score 265; DB 1, Length 387; 26.7%; Pred. No. 1.4e-10;
                 Local Similarity
tes 85; Conserv
Query Match
                     Best
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12 GGYLPSDSQDWPTIIPALLVAV~LVGFV~NI,CVIGILIHNAWKGRPSMIHSLIINI,SLAP 73

Gaps

154; Indels

Mismatches

53;

Conservative

Matches

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-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- PTM: THPRE CYSTEINE RESIDUES ARE FOUND IN THE C-TERMINUS, AT LEAST ONE OF WHICH MAY BE PALMITOYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE 58686393, PubMed 9425310;
Lorimer D D, Markowskj K , Renya P V ;
"Cloning, chromosomal location, and transcriptional regulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ( ·
                                                                                                                                                                                                                                                                                                                                                       : ·
· <u>×</u>
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19 GGWHPE - AUTUPLLFALIFUSTUSHUSHULAVILBGG QAUGTTH FILMIGUAD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AALFCLOWMFHALILOVWFSGFFLTRATYALRILUSHILVSYAMSOMMFHYALVSKHFRK
                                                                                                                   LSILLESARIEATAYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTITAVAKYTENTASTEA
                                                                                                                                                                                                  72 LCFILCCVPFQATIYTLDGWVFGSLLCKAVHFLIFLTMHASSFTLAAVSLRRYLAIRYFL
                                                                                                                                                                                                                                                                             GVENCLVPVFAVAEZFM
                                                                                                                                                                                                                                                                                                                                                       132 HSPBLR - TPRNALAAIGLIWGLSLLRSGF - VISYYPGSQLANLTV-HFAWSAFPFFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                      187 S. . . . MPGHLYELLAFGLELFFASFYFWBAYDQCKFFSTKTDMLRMCTFSKQTFSKQTTVMLMST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTOTPVESYLLPVIVIGLTYAPTLPYLWPAVPPV-AAGSGAPPAK-----PYVTFMTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 AIISALLMLEEWVANLWVWHLEAAGEAFF "GEIALS"VUMESISSANFILLEUNSEEFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metaloa, Chordata, Craniata, Vertebrata, Eutelonstomii
Mammalia, Butheria, Primates, Catarithini, Hominidae, Bomol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 45:496-508(1997).
Genomics 45:496-508(1997).
-- PROPRION SECRETED BY GENOME GALANIN. THE ACTIVITY OF PROPRION IS MEDIATED BY GENOMESIAS THAT IMPRITS ADENYIATE.
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Proc. Natl. Acad Soi "1 S.A. 91:9780-9783(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR 1995) to the EMB1/GunBark/BDP7 Astabades.
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Habert-Ortoli E., Amiranoff B., Loquet I., Laburthe M.,
Mayaux J.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human galanin 1 receptor gene (GALMIR).";
Riochem Riophys Pes, Commun, 241:558-564(1997).
                                                                                                                                                                                                                                                                        132 KQVSIHKYTIMSVLVA---IMTVASLLFLFEWFFSTIRHHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-077-2001 (Pel 40, Last annotation update)
3Albi re-eptor type 1 (GALI-R) (GALRI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 GERTICAGLIGRAFGRAS 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDAPD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Small intectine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Home sapiens (Human)
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                                                                      This SWISS-PROT outry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this categories to removed. Usage by and for commercial entities requires a license agreement (See Mttp://www.isb-sib.ch/announce/or cord an email to licensewich sib.ch).
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(POTENTIAL)
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InterPro, 1FRC0075, 3PGE_FL-Epst.

Pram, PE00001, 7W. 1F-FRH-1-1-3

PPOSTITE, PS00237, G_PPOTEIN_PERP_FL-1; 1

PROSTITE, PS00207, G_PPOTEIN_PERP_FL-1; 1

PROSTITE, PS00207, G_PPOTEIN_PERP_FL-1; 1

3 printing the control of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property of property 
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4 (POTENTIAL).

EXTRACELLICAR (FOTENTIAL).
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12 :ESTEMTIAL).
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CYTOFLASMIC (POTENTIAL).
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EMBL, U53511; AACS1936.1; -.
EMBL, U90658; AACS5397.1; -.
EMBL, U90658; AACS5397.1; JOINED.
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"was 88, Conservative
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This SWISS-PROT entry is copyright. It is produced through a condition between the Swiss Institute of Bioinformatics and the CYPT case of Bioinformatics Institution. There are no produce to the new many many in the produced by non-product institutions as land as the structure of the product is the constitution of the product of the structure of the product is the constitution of the product is the constitution of the product is the constitution of the product is the constitution of the product of the constitution of the product is the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the const
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Mammalia, Entherla, Rodentia, Sciuroquathi, Murile, Miriser, Estita
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InterPro; IPR00225; GPCR Rhodpsn.
Pfam; PFG-031; 7tm 1: 1.
PRINTS; PRG0237; GPCRRHODGENS
PROSTR: PSG0227; GPCRENS RECEP F1 1; 1.
PROSTR: PSG0222; GPCTEN RECEP F1 2; 1.
G-protein coupled receptor; Transmombrano; Glycopartons.
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STRAIN-Sprague Duwlby: Trouth Hypothelamus;
Waters S.M., Krause U.B.;
"Fat galaxie in engine 1 (601R2) coding request "coding and present the part of the 1 (601R2) coding request (601R2).
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Waids N., He C., Hesbari T., Payne M.;
Wholesdar closing of the rat galanta receptor type ."
Submitted Company to the part galanta receptor type ."
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FrMAIN
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Egypta (2007)
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3 (POTENTIAL).
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                                                                                                                                                                                                                                                                                              DREATE, 084914; QAQMZ2; 15-UL-1999 (Rel. 38, Created) 15-UL-1999 (Rel. 38, Last sequence update) 15-UL-1999 (Rel. 41, Last amposation update: Galanin Receptor type 3 (GALA-R) (GALA-R)
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                                                                           -PIDTPPS 343
The and and an active value of the Arabana Charles of the
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                                                                       321 Hİ PKPSHIĞBTKENKS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALES OR GALNES.
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                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 ALLWLPEWVAWLWVWHLKAAGPAPPOGFIALSQVLMFSISSANPLIFLVMSEEFREGLKG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 140 RAAVGLVWLLAALFSAPYLSYGTVR-YGALELCVPAWEDARRRALDVATFAA-----G 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 KLYPL----LAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLLSIAIIS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 YLLEVAVVSLAYGRTLCF----LWAAVGPA---GAAAAEARRATGRAGRAM-LAVAALY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 AAIYTLDAWLFGAFVCKTVHLLIYLTMYASSFTLAAVSLDRYLAVRHPLRSRALRTPRNA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                   83 ATAYSKSVWDLGWPVCKSSDWFIHTCMAAKSLTIVVVAKVCFMYASDPAKQVSIHN-YTI 141
                                                                                                                                                                                                                                                          53; Mismatches 155; Indels 60; Gaps
                                                                                                                                                                                                                                                                                            26 IFALLVAVCLVGFVGNLCVIGILLH...HAWKGKFSMIHSLILNLSLADLSLLLFSAPIR 92
                                                                                                                                                                                                                                                                                                                           20 VÉVIFALIFLIGMVGNGLVLAVLLQPGFSÁMQEPRSTTDLFÍLNLAVÁDLCFILCCVPFQ 79
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!- SUBCELLULAR LOCATION: Integral membrane protein.
!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vortebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129/Sv, Kolakweki L.F. C., C'Neill G.P., Howard A.D., Broussard S.R., Rolakweki L.F. C., C'Neill G.P., Howard A.D., Nguyen T., Kargman S. Sulivas B. V. Feighner S.D., Sawrdargo M., Nguyen T., Kargman S. Shiao L.-L., Hreniuk D.L., Tan C.P., Evans J., Abramovitz M., Chareauneuf A., Coulombe N., Ng G., Johnson M.P., Tharian A., Khoshbouei H., George S. P., Smith P.G., O'Dowd B.F., Tharian A., Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POSPERHEHEAHPALPEV@PASSGPAGYPGDAPP 342
                               CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
PALMITATE (BY SIMILARITY).
POLY.ALA.
                                                                                                                                                                                                                         Length 370;
                                                                                                                 R -> S (IN REF. 3).
F -> Q (IN REF. 2).
R -> P (IN PEF. 2).
R -> C (IN REF. 2).
W, CE5B39B6147AFAD4 CRC64;
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                       12.0%; Score 261; DB 1;
24 5%; Pred No. 2 4e 10;
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15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Galanin receptor type 3 (GAL3-R) (GALR3).
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                7 (POTENTIAL)
                                                                                                                                                                                          40410 MW;
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088853;
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                               DOMAIN
CARBOHYD
DISULFID
DOMAIN
TRANSMEM
                                                                                                                                     CONFLICT
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 YLLDVTVVSLAYGPTLCF----IWAAVGPA---GAAAARAPPATGPAGPAM-LAVAALY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 KLIPL ---- LAFGLEFFASFTFWRAYEQCKFRGTKTGNLENGIEGRGYTWLLSIAIIS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 ALLWLPEWVAWLWWHLYAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEFFESLYG 30A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Saps
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                                                                                                                                                                                  PFam; Provoca, ...
PRINTS, PROCEST, GFCPPHONOBSN.
PROSITTE, PSOCEST, G PROTEIN RECEP F1 1; 1.
PROSITTE, PSSOCES, G PROTEIN RECEP F1 2; 1.
G-proceein coupled receptor; Transmembranc, Glycoprotein;
Miltigene family; Lipoprotein; Palmitate.
Miltigene family; Lipoprotein; BAImitate.

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7 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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24.4%; Pred. No 2 66-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (POTENTIAL)
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                                                                                                                  MGD; MGI:1329003; Galr3.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                      EMBL; AF042783; AAC36588.1; -.
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370 AA;
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Best Local Similarity
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15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-2002 (Rel. 41, Last annotation update) Galanin receptor type 1 (GALS-R) (GALR³)

Homo sapiens (Human)

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REP. MEDILE-2005/165; Pubmed-10591208.

RA Chang M. Gmirk Lid., Alisecush R., Almeida J.E., Babbige A.K., Chang M., Gmirk Lid., Alisecush R., Almeida J.E., Babbige A.K., Radyuley C., Balley J.E., Briddeman A.M., Buck D., Bulgess J., Radyuley C., Bulley S.E., Briddeman A.M., Buck D., Bulgess J., RA Burd C.P., Blakey S.E., Briddeman A.M., Buck D., Chen Y., Clark G., Radvilly R.D., Cohlin B.E., Chen Y., Clark G., Collin B.E., Chang S.M., Cobbey V.E., Colder C.G., Collin B.E., Chang S.M., Cobbey V.E., Colder C.G., Collin B.E., Chang R.E., Edwill R.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Millians S.A., Milliams S.A., Milliams S.A., Milliams S.A., Milliams S., Robers J., Shimizu N., R.A. Shint B.E., Chen B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Collin B.E., Col
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This SWISS-PROT entry is copyright. It is produced to an a condition between the Swiss Institute of Bioinformatics and the FVE creative to the European Richformatics Institute. There are no copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright in a copyright i
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140 RAAVGI.VWILAALESAPYI.SYYGTVR-YGALEL@VPAWEDARRALDVATFAA···· G 192
                                                           191 FLYPL----LAFGLFLFFASFYFWPAYEQTERFORFTON PNOIPSMOUTOMLSIALIS 244
                                                                                                                      SAAAAEAFFFATTFAGFAW - I.AVAATT 244
                                                                                                                                                                              247 ALLWIPEWVAWIWVWHIKAAGPAPPQGFIALSQVIMFSISSANPLIFLVMSEEFFEGLKG 306
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01-APR-1993 [Bel. 25, Created)
01-NOV-1995 [Bel 32, Last sequence update)
16-OCT-2001 [Rel. 40, Last annotation update)
Prohable G protein-coupled receptor GPR72 precutsor (Glucocorticoid-
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Eukaryota, Metarba, Chordata, Craniata, Vertekrata, Eufeleostomi.
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Nus.
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Ptam, PF00001, 7tm_1, 1.
PFNITS, PF00227, GPCFERHOUSEN.
PPOSITE; PS00237, GPECTEIN RECEP_F1 1, 1.
PPOSITE; PS00262, G_PROTEIN_RECEP_F1 2, 1.
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POTENTIAL.
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2 (POTENTIAL).
EXTRACELLULAP (POTENTIAL)
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MGD; MGI:95712; Gir
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Bukaryota: Metarca, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Euthoria, Rodentia, Hystricognathi, Cavildae, Cavia.
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                                                                                                                                                                                   FOTENTIAL POTENTIAL
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MISSING (IN ISOFORM RP39)
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                                                    CLAR (FOTENTIAL)
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                                                                                       CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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MEDLINE-92256438, FubMed=1374648;
Gorbulov V., Abbundova A., Luzius H., Fahrenholz F.:
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N-LINKED (GLCNAC...)
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3 (FOTENTIAL) CYTOPLASMIC (FOTENTIAL) 4 (FOTENTIAL).
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 26, Last semuntation update)
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TACRLOR TACIR.
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                                                                        (FCTENTIAL)
                                                                                                                                              7 (FUTENTIAL)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the FMME outstallen the European Richformatics Institute. There are no restrictions on its use by non-profit institutions as larged as its content is in no way modified and this standard where the source of the second and this standard and this standard and this standard and the second and this standard and the second and this standard and the second and this standard and the second and this standard and the second and and this standard and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the se
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22.1%; Ried. Ma. 2.5c 98;
[VM - 80; Mismatches 159; Indels 64; Gaps
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REAL MEDIUS 2009 165; PubMed=10691288; Brickhowich Fileston N F Contham I. Hunt A.E., Collins I.E., Shrekhowich Fileston N F Collins I.E., Almerida J.E., Stirk H. J., Almerida J.E., Almerida J.E., Stirk H. J., Almerida J.E., Almerida J.E., Stirk H. J., Almerida J.E., Stirk H. J., Almerida J.E., Stirk H. J., Almerida J.E., Shrekhowich R.E., Shrekhowich R.E., Shrekhowich R.E., Shrekhowich R.E., Shrekhowich R.E., Shrekhowich R.E., Shrekhowich R.E., Shrekhowich R.E., Shrekhowich R.E., Shrekhowich R.E., Shrekhowich R.E., Shrekhowich R.A., Milliam R.E., Hall-Tamlyn C., Horthowich R.A., Milliam R.E., Manglerd R.E., Shrekhowich R.A., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.E., Milliam R.
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Curness C.E., Cemilly, D.L., Sestan F., Ten T. F. Y.,
Stikant C.E., Rent G., Partel Y.C., Niznik H.H.,
"A buman somatostatus receptor (GSTRN), located in the performance displays preferential affinity for sematostatus (4.18° performance).
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01-0cT-1994 (Pel. 27, Cheated)
0CT-1994 (Pel. 27, Lest sequence update)
1-1TH 2002 (Pel. 41, Lest amoutation update)
Somatostatin receptor type 3 (SSRR) (SSR 28).
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MEDLINE-93149123, PubMed-1337145,
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SSR3_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Gyres M., Du., Fulton L., Gola D., Graves T., Hawkins J., Scheet M., Eutreille P., Layman D., Ozersky P., Rohlfing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J., Korf I., Bedell J.A., Hiller L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., Kim Chim M. C., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Than N., Wright H.;
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PURCTION. PECEPTOP FOR SOMATOSTATINS 14 AND -28, THIS PECEPTOR 18 COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION Integral membrane protein.
TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.
SIMILARITY: BELUNGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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N-LINKED (GLCNAC. .) (POTENTIAL).
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PRINTS, PR00237, GPCRRHODDSN.
PROSITE, PS00237, GPROTEIN RECEP_F1 1, 1.
PROSITE, PS50262, GPROTEIN RECEP_F1 2, 1.
G-protein coupled receptor/Transmembrane, Glycoprotein,
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EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL) .
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EMBL; Z82188; CAB45263.1; -.
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HSSP; P34996; 1DDD.
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SEQUENCE 418 AA, 45847 MW, 1227095F80119004 CRC64;

Query Match
Best Local Similarity 23.4%; Pred. No. 3.4e-08; Indels 48, Gaps 11;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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  *** SSPWFINTOWAARSLTTGTVARTTFNYKETEKEV 134
                                                                                                                                                                                                                                                               252 PEWVAWLWYWHIKAAGPAPPO -- GFIALSQVLMFSISSAMPLIFIVMSFEFFEELETY 307
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-!- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO TACHYKININS IS: SUBSTANCE P > SUBSTANCE K > NEUROMEDIN K.
-! SIMILARITY: BELONGS TO FAMILY 1 OF G PROTEIN COUPLEU KEUEPIORS.
                                                                                    135 SIHNYTIWSVLVAIWTVASLLPEPERFSTIRHHEGVEMCHVDVPAVAEEFMSMFGKLYF
                                                                                                                              162 -----TVSAAVWVASAVVVLPVVVFSGV--PRGMSTCHMQWPEPAAAWRAGFTTYTA
                                                                                                                                                                                                                212 ALGPEGELLVICLCYLLIVVKVRSAGPRVWAPSCOPPERSERFVTRMVVAVVALLEVICWM
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                                                                                                                                                                        195 LLARGIPLEFASFYFWRAYDQCKKRGTKT---QMLPMQTPSYQVTVMLLSIALISALLWL
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                     103 QNALSYWPFGSLMCRLVMAVDGINOFTSIFCLTVMSVDRYLAVVHFTRSARWRTAEVAR
                                                                                                                                                                                                                                                                                                    272 Prykmi - . . vrvychiheepaffchyfivvalfianscamfilligflisykfrosfr
                                                                                                                                                                                                                                                                                                                                                   308 WKWMITKKPPTVSBSQETPAGNSBCLPPKVPSPESPASIPEKEKPSSPSSGKSK 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular evidence that granuloma T lymphocytes in murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Fel. 25, Created)
01-APR-1993 (Fel. 25, Last sequence update)
30-MAY-2000 (Fel. 39, Last annotation update)
Substance-P receptor (SPR) (NK-1 receptor) (NY-1R).
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STRAIN=CBA; TISSUE=T-cell, and Brain;
MEDLINE=94165478; PubMed=8120392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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85 AYSKSVWDLGWFVCK----
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22.6%; Pred. No. 4.50 08;
tive 70; Mismatoneo 165; Indele 64; Saps
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BMBL, (27826; AAA17891.1; -. PTR, $20394; S20304.
MGD, MGL198475; Tacri.
Interior, IPPROPAGE, GPCP_PLOSES.
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01-AFR 1990 (Rel. 14, hast sequence update)
15 JUL 1999 (Rel. 36, Last annotation update)
13 JUL 1999 (Rel. 36, Last annotation update)
13 JUL 1999 (Rel. 36, Last annotation update)
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Mammalia, Butheria, Rodentia, Sciurognathi, Murciae, Murcie, Elfus,
NCRI_TaxIP-10116,
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Tokena Y., Sasai Y., Tanba K., Fujiwana T., Tonchi H. F.,
Shigomete R., Pakinka A., Onbibo H., Nabanishi K.,
"Walo-lai dana medinatis of ifigurosal shwiitini dan isini sh
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MEDLINE-OF161991, PubMod-2154852;
Hershey A.D., Krause U.E.;
Hershey A.D., Krause U.E.;
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MEDLINE 91154239, DubMed.1705552,
Herehey A.D., Dykema P.E., France J.E.;
"Cryatication, Strattle, and expression of the processing strattle,").
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PRINTS; PR0237; GPCRRHOLOPSN,
PROSITE; PS00237; GPROTEIN RRCH F1 1; 1.
PROSITE; PS00237; GPROTEIN RRCHP F1 2; 1.
G-protein compled to Peprote; Transmombiance Signification, Phosphorylation; Lipoprotein; Palmitate.
Phosphorylation; Lipoprotein; Palmitate.
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EMBL, M64233; AAA42176.1; UGINED.
EMBL, M64233; AAA42176.1; UGINED.
EMBL, M64234; AAA42176.1; UGINED.
EMBL, UGSO97; AAA42176.1; UGINED.
EMBL; UGSO97; AAA42176.1;
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Pattus norvegiqus (Rat).
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Hershey A.D.;
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01-APP-1993 (Pel. 25, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Netromedia Proceptor (NPP) (Neurrhinin R reseptor) (NP-4 1000gt)
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
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                       EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLITAR (POTENTIAL).
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"Expression cloning of CDNA encoding a seven-holix
human placenta with affinity for opioid ligands.";
Proc. Natl. Acad. Sci. "1 S. A. 99-4124 4129 (19-2).
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This CWISS-FFOT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bacinformatics and the EMEL outstands the European Bloinformatics institute. There are no estructions in the type on it fit institutions as long as its intent, a in no way wouldied and this statement is not removed. These by and for communication that the statement is not removed. The same for communication send an email to licensealsb-sub.ch).
                                                                                                                            --- SUBCELLULAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: HIGHEST LEVELS IN SKELETAL MOSCLE, LIVER,
--- LUMA AND HEART. LOW LEVELS IN PANCHEAS.
--- SIMILARITY: FELONDS TO FAMILY 1 OF G-PROTEIN GUIDLEL MECHATORS.
HIGHEST TO OTHER TACHYKININS RECEPTORS.
--- CAVITION, Was originally (Ref. 1) thought to be a kappa-type cycoli
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Tarefrey, IPP677276, GPCF_Phedgen.
Firetroy IPP67777, Tem_1, 1.
PPINTS, PP67777, GPCFPRODESN.
PROSITE, P860237, GPROTEIN RECEP_F1_1, 1.
PP681TE, P880767, GPROTEIN PECEF_F1_2, 1.
Pp681TE, P880767, GPROTEIN PECEF_F1_2, 1.
Donaldson L.F., Haskell C.A., Hanley M.R.;
"Functional characterization by heterologous expression of a movel
cloned tachykinin peptide receptor.";
Biochem. J. 320:1-5(1996)
--- FUNCTION THIS T.A. REPERTOR FOR THE TATHIFFILM MEN'S SERFITHE
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PECEPTOR IN TATHIFFORMINS IS: NEUPOMEDIN R. SUBSTANCE R. SCHOLAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTINUE SYSTEM: Windows SOFTWARE: FASCER (1) Windows SOFTWARE: FASCER (1) Windows SOFTWARE: FASCER (1) Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/993.088A FILING DATE: 18-DEC-1997 CLASSIFICATION: 530 PROPERTY TO DATA: APPLICATION NUMBER: 60/033,851 FILING DATE: 27-DEC-1996 ATTHENDY ARET: THEORYMATICH: NAME: Heber, Sheldon ORESTRATION MINRER: Abeldon ORESTRATION MINRER: Abeldon ORESTRATION MINRER: Abeldon ORESTRATION MINRER: Abeldon ORESTRATION MINRER: 39,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tan, Carina
APPLICANT: Tan, Carina
APPLICANT: Sullivan, Kathleen
TITLE OF INVENTION: MACLEOTIDES FNCODING SAME
KINGEP OF SETTINGS 20
CORRESPONDENCE ADDRESS:
                       US-09-058-333A-2
US-09-058-333A-4
US-09-058-333A-4
US-09-058-333A-4
US-08-417-103-10
US-08-417-103-10
PCT US-08-417-103-10
US-08-430-286A-9
US-08-090-369-1
US-08-971-1
US-09-971-1
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STREET F F E X 2000, 12F E Linelle Ave.
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 9, Application US/08993088A; Patent No. 6297855; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOOKET NIMMRED: 19846
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ZIP: 07065-0900
COMPUTER PRADARLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
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LENGTH: 371 amino acid
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                                 INFORMATION FOR SEC IN NO.
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US-08-993-088A-9
   TELEX:
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US 08 993-424B-9

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72 USILLESAPIPATAYSKSUWDLGWFVÇKSSDWFIHTGMAAKSLTIVVVAKVCPMYASDFA 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 FKITASLIPPAPPPASGPUCILAPSHESGSMLE----PESTELTQVSEAAGFLUVA---- 354
                                                                                                                                           71 LCFILCCVPFQATIYTLDDWVFGSLLCKAVHFLIFLTMHASSFTLAAVSLDRYLAIRYFM 130
                                                                                                                                                                                            132 KQVSIHNYTIWSVLVA.--IMTVASLLPLPEMFFSTIRHHEGVEMCLVDVPAVAEEFMSM 188
                                                                                                                                                                                                                                       131 HSPFLR--TPRNALAAIGLIWGLALLFSGPYLSYYSQSQLANLTVCHPAWSAPRRAMDL 188
                                                                                                                                                                                                                                                                                        189 ----FGET YPLLAFGLPTFFASFYFWPAYDQGBEFFGNLPNGIPSEGVTVMLLSIAI 244
                                                                                                                                                                                                                                                                                                                                       189 FTEVESYLLEVLVISLIPYARTLHYLWPTVIPV-AAGSSSGPAR-----BYVTPMIVIVAV 242
                       10 GTYLPSDSQDWPTTIPALLVAVGLVSFVSNLGVISILLHNAWKGKPSMIHSLILNLSLAD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tan, Carina
APPLICANT: Kolakowski, Lee F., Jr
TITLE OF INVENTION: MOUSE CALANIN PROEPTOR SALEZ AND
TITLE OF INVENTION: HUTLECTIPES FUNCOUS SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITM TYPE Clakere
COMPUTER: IRM Comparible
OPERATING SYSTEM: Windows
SOFTWARE: Fast SEQ for Windows Version 2 Ob
CHERENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,424B
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O Pox 2000, 124 E Lincoln Ave
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18-DEC-1997
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Patent No. 6337206
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FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION.
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TELECOMMINICATION INFORMATION:
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TYPE: amino acids
TYPE: amino acid
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TOPOLOGY: line:
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PRIOP APPLICATION DATA.
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ZIP, 07045 0400
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US-08:993-424R-9
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APPLICANT: Branchek, Theresa A.
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TITLE OF INVENTION, MOTIENTINES ENGLING SAME
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SCETWARE TABLES FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,424B
FILLING DATE: 18-DEC-10-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merck & Co., Inc.
O Box 2000, 126 E linocla Ame
155 VSFIWALSIAMASPVAXYQELFHEDSMCTFUWSKWP-
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PRICE APPLICATION DATA:
FAPILICATION NUMBER: 60/033,851
FILING DATE: 27-DEC-1996
ATTORNEY/ADELT THEOFMATION
NAME: HORDER, Sheldon O'REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                         221 · · · CNESPHGDAKE KANIDTOPS 340
                                                                                                                                                                                                                          318 TVSESQETFAQUSECLPDKVPSPES 342
                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/08993424E; Patent No. 6337206; GENERAL INPORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER PEADAPLE FORM-
MEDIUM TYPE: Diskette
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MOLECULE TYPE: protein
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ZIP: 02065-0900
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                                                                                                                                                                                                                                                                                                                                 RESULT 5
US:08:993:424B-3
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                                                                                                                       268 AEF.-GAFPLTPASFPFRITAHCLAYSNVRIIYAFLSENFPKAYKQVFFGPV---- 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 MOULTHSELTITULARSE PSPERSTITLEILMESTARTLARTLEFOLPROATUVALETAVUS 133
           200. LPLEFASSYFWPAYP@CKFPGTFTTQNLRNGTESF@VTVWLLSIAIISALLWLPEWVAWLW 359
                                                 200 I.PII.LITCPOYAFVIAHIHPP-LPNMSPRSEASPRPTAQOVIAVVVPSISWI.PHVIHIM 267
                                                                                            260 VWHUKAAGPAPPQGFI--ALSQVDMFSISSANPLIFLVMSEEFPEGLKGVWHWMITKEPP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 WEVOKSSIMFIHTOMAAKSLTIVVVAKVOFMYASIPAKQVSI-HNYTIWSVI,VA----- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEFTISMIVELFILAAMSUEFTVAIVHSPRSSSLFVSFNAILG 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%, Score 269.5, DB 4, Length 346,
27.1%; Pred. No. 1.5e-14;
tive for Mismatches 130; Indels 47; Saps
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tan, Carina APPLICANT: Sullivan, Kathleen TITLE OF INVENTION: GALANIN PECEPTOP GALP2 AND TITLE OF INVENTION: WUCLEOTIDES ENCODING SAME WIMBER OF SECTIONS 20 CORRESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE. FASTERO for Windows Version 2.0b
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: P.O. Box 2000, 126 E Lincoln Ave
Rahway
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PRIOR APPLICATION DATA:
APPLICATION TIMBER: 60/33,851
FILING DATE: 27.DEC 1996
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
PEGISTFATION NIMPER: 38,179
                                                                                                                                                                                                            321 -- CNESTHODAKE PURIDIPPS 340
                                                                                                                                                                               318 TVSESQETPACHSECLPDFVPSPES 342
                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08993088A
Patent No. 6287855
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594 1958
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IRM Compatible
SYSTEM: Windows
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Matches 88, Conservative
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                                                                                                                                                                                                                                                                                      RESULT 4
US-08-993-088A-3
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36 VGFVGRLCVIGILLHRAWEGKF SMIHSLILHLSLACLSLLLFSAFIRATATCHSSVWDLG 94
                                                                                                                          95 WEVINSSTWITHTHINAMESTITIVIVARIVERMESTRALIVEL HITTERSTUAL ---
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148 ---IWTVASLLPLPEWFFSTIRHHEGVE-MCLVDVPAVAEEFWSMFGKLYPL--LAFG-- 199
                                        195 VORIWALCIAMASPVAYYOPLEHPROMOTEÓWEBWP - MOLHFFAYVVOTEVEGYL 108
                                                                                                                                            209 LPLLLICFCYAKVLNHLHKK-LKNMSKKSEASKKKTAQTVLVVVVVFGISWLPHHVIHLW 267
                                                                                                                                                                                          240 VWH1KAAGPAPPGGFI--ALSQVIMFSISSANPLIFLVMSEEFREGLKGVWKWMITKKPP 317
                                                                                                                                                                                                                   12.4%) Score 260.5) DB 4, Length 346,
27.1%; Pred No 1 co.14;
ive 60, Mismatches 130, Indels 47; Cags
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                                                                                          200 IPLEFASEYEWPAYOTYYFEGIYTTMLENGIPSYOUTVMLISIAIISALLWLPEWVAWLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bard, Jonathan A
APPLICANT: Berowsky, Beth
APPLICANT: Smith, Kallis
TITLE OF INVENTION: AND USES THERBOP
TITLE OF INVENTION: AND USES THERBOP
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CURRENT APPLICATION DATA
APPLICATION NUMBER US/03/058,333A
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                                                                                                                                                                                                                                                                                       318 TVSPSOETPAGNSEGLPPKVPSPES 342
                                                                                                                                                                                                                                                                                                                                    321 ----CNESPHGDAKE-KNRIDTPPS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09058333A Patent No. 6168812
GENERAL INFORMATION:
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REGISTRATION NIMBER: 28,678
PEFERENDE/CVET MINESES COT
TELEPHONE: 712 778 0400
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INFORMATION FOR SEQ ID NO: 5:
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
TOPOLGGY: linear
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY - linear MOLECULE TYPE: DNA
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Best Local Similarity
Matches 99, Conserv
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STREET: 110
TTV: NOW YORK
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148 ---IWTVASLLPLPEWFFSTIRHHEGVE-MCLVDVPAVAEEFM3MF3KLYFL LAF-1 33
                                     MULHER ATTA TEMPERS 1. 18
                                                                        200 IPLPPASPYPWPAYPQTKFESTFTONIPNOIPSEOVTVMILSIATISETAMTSEWVAWGW 199
                                                                                                                                                        260 VWHLKAAGPAPPOGFI -- ALSQVLMFSISSANPLIFLVMSEEFREGT EGVWFWMITTKFIT 117
                                                                                                                 200 LPLLLIOPTYAPVINHUHPF (Phrysprotacphycherus)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fujii, Ryo
APPLICANT: Obtaki, Tetsuya
APPLICANT: Fukusaki, Shoji
APPLICANT: Kazuhiro
IITLE OF INVENTION: S PROTEIN COURTED PEOPUTOR INTERIOR
IITLE OF INVENTION: PROTUCION, AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. DIME, BROMSTEIN, RORPETO & CUGHMAN, 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: FC.1058/MS-DOS
SOPTWARS: Patentin Release #11.0, Vorsion #11.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/04/$13,9748
                                     185 VGFÍWALSIAMASFVATTORLFHFRANGIFARRIMÉ
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PRIOR APPLICATION DATA:
#PLICATION NIMMET
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PPIOR APPLICATION NUMBER: JP 6 180077
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PPIOP APPLICATION DATA:
APPLICATION NATA:
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; Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: HINDMA, Shuji
                                                                                                                                                                                                                                                                            321 ---- CNESPHGDAKE-KNRIDTPPS 340
                                                                                                                                                                                                                                       318 TVSESQETPAGNSEGLPDKVPSPES 342
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PRIOR APPLICATION DATA:
APPLICATION NATA:
APPLICATION PATA:
FILING DATE:
APPLICATION NUMBER: JP 7-07
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N: 536
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-
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PRICE APPLICATION DATA:
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PRICE APPLICATION DATA:
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Hosoya, Masaki
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APPLICATION NUMBER.
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STREET: 10.
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US-08-513-974B-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 VGPIWALSTAMASPVAYHOPLFHRRSNOTFFWEGWF-----NYLHYMAYVVTPVFGYL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gars
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 WEVCKSSOWFIHTCMAAKSLTIVVVAKVCFMYASDPAKQVSI-HNYTIWSVLVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                       Overy Match 12.4%; Score 269, DB 3, Length 348; Best Local Similarity 28.3%; Pred. No. 1.6e-14; Matches 87; Conservative 54; Mismatches 128, Indels 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Tan, Carina
APPLICANT: Tan, Carina
APPLICANT: Sullivan, Fathleen
TITLE CF INVENTION GALAHIN PECEPTOF GALFL AND
TITLE CF INVENTION. WOLLECTIDES ENCODING SAME
NUMBER OF SEQUENCES: 20
COPPERFONDENCE ANDPESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Merck & Co., inc.
STREET: P O Rox 2000, 126 E Linceln Ave
FILING DATE: 11-AUG-1994
PPIDE APPLICATION DATA
APPLICATION WIMBEN. JF 6 180273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION WIMBER. JF 6-189272
FILING DATE: 11-AUG 1994
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
1/8-08-993-088A-10
/ Sequent 0. Application 75/08993088A
/ Parent No. 6287855
                                                                                                                                                                                          45753
                                                                                                                                                   NAME: FESNICK, David S. REGLESTRATION NUMBER: 34,235 REFERENCE/DOYKET NUMBER: 45' TELECOMMINICATION INFORMATION.
                                                                                                                                                                                                                                                TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 46:
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MOLECULE TYPE: peptide
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Best Local Similarity 28.3%; Prod. Mo. 1.6e-14;
Matches 87; Conservative 54; Mismatches 128; Indels
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GENERAL INFORMATION:
AFELICANT: Tain, Carina
AFELICANT: Kolakowski Lee F., Jr.
TITLE OF INVENTION: MOUSE GALANIN RECEFFUR SALEL AND
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: 120
SOFTWARE: FASTSEQ for Windows Version 2.0b
CYPERT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,088A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 530
FRIOR APPLICATION: ATALA
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STPERT: P O POX 2000, 126 E Lincoln Ave.
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Patent No. 6337206
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TELEPHONE, 732-594-1958
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SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
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TELEFAX: 732-594-4720
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MEDIUM TYPE: Diskette
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COUNTRY, US
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NUMBER OF SEQUENCES: 17
COFFECEDINGENCE ADDRESS:
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Best Local Similarity 28.3%; Pred. No. 1.60-14;
Mitches 87; Conservitive 54; Mismatches 109; Infals 19, Gaps
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                    OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/38/993,424B
FILING DATE: 18-DEC 1997
CLASSIFICATION: 536
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Patent No. 6399325
                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. (13.2, 95.)
FILING DATE: 27 DEC 1996
ATTORNET/AGENT THE GRANTICH.
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                            REFERENCE/FOCKET NUMBER 19
PELBCOMMUNICATION INSESSMATION:
TELEPANE 732-594-1958
TELEFAX: 732-594-4720
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APPLICANT: FURISIMI, Shoji
APPLICANT: OHTAKI, HESEUYA
APPLICANT: HOSOYA, MASAKI
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
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APPLICANT: ONDA, Haruo
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MOLECULE TYPE: protein
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APPLICANT: FUJII,
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  COMPUTER:
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28.3%; Pred. No. 1.6P 14;
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                                                                                                                                                                              | Sequence 44., Application us/085;1974B
| Patent No. 6114139
| GEMERAL IMPROMATION:
| APPLICANT: Hindma, Shuii
| APPLICANT: Historya, Kasaki
| APPLICANT: Pujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 6 326637
FILING DATE
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PEFERINF (DOCKET NIMBER: 45,
TELECOMMUNICATION INPERMATION:
TELEPHONE: 617-523-6440
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Fujii, Ryo
Ohtaki, Tetsuya
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER. IRM Compatible OPERATING SYSTEM: DOS
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APPLICATION NUMBER: 6-247
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MOLECULE TYPE: Peptide
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MEDIUM TYPE: Diskett
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TOPOLOGY Linear
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Best Local Similarity
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HS-A8-513-9748-343
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46 MGVLGMSLVITVLARSF PGEFFSTWLFILMLSIANLAKILFGIFFGATVYALTFWVIG 104
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25.1%; Fred. No. 2.2e-14;
Live 60; Mismatches 174; Indels 44; Says
                                                                                                                                                                                                                                                                                                            105 APICK----FIH-----YPPTVSMLVSIPTLAAMSVDRYVAIVHSBRSSSSLRVSRNALLS 15
                                                         36 V3FVGHIGHTSTLIHNAMKGMP SMIHSLITHUSLACTSCLUFGARTBADAYDRSTWOLG 34
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                                                                                                                                                                                                                                              95 WEVÇESSEWPIHTIMAAESLIIVVVARVOEMYASDEFARQVSI-HMYIIMSVLVA-
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APPLICANT: Blockquist, Brian T. , McCaleb, Michael L.;

APPLICANT: Confideld, Linda J., Yoo-Warren, Heeja

TITLE OF INVENTION: Salanin Perepres and Nucleic Acid

TITLE OF INVENTION: Sequences

NUMBER OF SEQUENCES: 4

COPPESPONDENCE ADDPESS:
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IBM PC Compatible
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APPLICATION WORBER: US/08/665,034A
FILLING DATE: 5 JUN-1996
AUTORNEY/AGENT INFERMATION:
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TOPOLOGY: Linear
IMMEDIATE SOURCE:
Clone FME77 amino acid sequence
US:08.665 034A.2
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REJISTRATICH NUMBER 22888
PERFERENCE/GOCKET NUMBER: WH S012-Orig.
TELECOMMUNICATION INFORMATION:
TELEPHONE. (202) 812 2705
INFORMATION POP FOR 11 NO. 2.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09665034A Patent No. 6410686
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MEDIUM TYPE: Diskette
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US-08-665-034A-2
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APPLICANT: Fukusumi, Shoji
APPLICANT Obgi, Katukito
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOR
NUMBER OF SEQUENCES: 380
CORPRESPONDENCE ADDRESS:
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130 Water Street
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APPLICATION NIMBER: PCT/JP95/01599
FILING DATP: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
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PRIOR APPLICATION NUMBER: JP 6-236357
APPLICATION NUMBER JP 6-33637
FILING NAME OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A PRICE OF A 
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-27017
FILING DATE: 02 NOV 1994
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FILING DATE: 11-AUG-1945
PRIOP APPLICATION TATA.
FILING DATE: 10 6-189272
FILING DATE: 11 AUG 1944
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP 7-057186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77P 7-007177
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SEQUENCE CHARACTERISTICS:
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FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-1994
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PRIOR APPLICATION DATA:
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617-523-6440
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PRIOR APPLICATION DATA:
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11. ELELLERSAR IBATAKORSVAK LEMPVEYOSSPAPIRITYAAFSCTIVVVAFVOPATASEP 190
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                                                                                                                                                                                                                                                                                                                   131 ARCYSTRNYTIWSVLVA---IMTVASLLPLPEWPPSTIPHHE--GVEMCLVNVPAVABEF 145
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APPLICANT: Smith, Kelli E.
APPLICANT: Smith, Kelli E.
APPLICANT: Gerald, Chicache P.G.
APPLICANT: Unomeyer, David
APPLICANT: Unomeyer, David
APPLICANT: Fornay, Theresa
APPLICANT: Fornay, Callos
TITLE OF INVENTION: DNA ENCODING A MAMMALIAN
TITLE OF INVENTION: DNA USES THERESE
MUMBER OF SEQUENCES: 14
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COMPUTER: THM PC compatible
OFFICER CONTENT FOR STORY ME DOS
SOFTWARE: Perenth Fellows HI O, Version HI NO
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1185 Avenue of the Americas
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ATTORNEY/ABENT INFLEMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPREDENCE/CT FET HUMBER: 27233
TELECOMMIN CATTON INFLEMATION:
TELEPHONE: 212-278-9490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-391-0525
INFORMATION FOR GEQ 1D NO. 8.
SEQUENCE CHARACTERISTICS:
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FILING DATE:
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                                                                                                                                                                                                                                                                                                11 AGGYLFSDSODWRTIIPALLWAVCLVGFYQULYLGLLHHVARF ETLOKIE'T LUKLI'A
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Chery Watch
Best Local Similarity 25.1%; Pred. No. 2.66 14;
Watches 93, Crestrative Co. Wirmprober 174; This.s
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APPLICANT: Fan, Carina
APPLICANT: Sallivan, Kathleen
TITLE OF INVENTION SALANIN PROFESSION CALRY AND
TITLE OF INVENTION, NUCLECTIONS ENTING SAME
NUMBER OF SEQUENCES: 20
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COMPUTER IN Compatible
OPERATING SYSTEM. Windows
OPERATING SYSTEM. Windows
WINDOWS WINDOWS
THREW AFFLICATION DATA:
APPLICATION NUMBER: US/OR/993,048A
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P.O. Box 2000, 126 E. Landoln Ave
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; Patent No. 6287855
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APPLICATION NUMBER: 60/03,851
FILLY PATE: 27-PFC 1996
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TELEPHONE: 733-594-1958
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INFORMATION FOR SEC IB NO-
TECHNOR CHARACTERISTICS:
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TELEPHONE: 732-504-4720
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ZIP: 07065-0900
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 KTEKAEIPILF 371
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CLASSIFICATION:
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STREET: F...
TTV: Rahway
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US-08-993-088A-2
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12.3%; Score 267; DB 4; Length 372;
25.1%; Pred. No. 2.6e-14;
ative 60; Mismatches 174; Indels 44; Gaps 11;
                                                                                                                                                                                                                                                                                                             71 DLSLLLFSAPIRATAYSKSVMDLGWFVCKSSDWFIHTCMAAKSLTIVVVAKVCFMYASDP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                     131 LHSRELR--TPRNALAAIGLIWGLALLFSGP--YLSYYROSOLANLTVCHPAWSAPRRRA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 MSM----FGKLYPLLAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLLS 241
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                                                                                                                                                                                                                            11 AGGYLPSDSQDWRTIIFALLVAVCLVGFVGNLCVIGILLHNAWKGKPSMIHSLIINLSLA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 IAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEFR 301
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                                                                                                                                                                                                                                                                  18 SGGWOPE-----AVLVPLFFALIFLVGTVGNALVLAVLLRGG--QAVSTTNLFILNLGVA 70
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APPLICANT: Tan, Carina
APPLICANT: Kolakowski, Lee F., Jr.

ITLE OF INVENTION: MOUSE GALANIN PECEFTOR GALR2 AND
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
TITLE OF ENVENTION: NUCLEOTIDES ENCODING SAME
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APPLICATION NUMBER: US/08/993,424B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Merck & Co., Inc.
P.C. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JMBER: US/08/993,424B
18-DEC-1997
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REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 19846NP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08993424B
Patent No. 6337206
GENERAL INFORMATION:
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FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
LENGTH: 372 amino acids
TYPE: Amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                    93; Conservative
                                                                         MOLECULE TYPE: protein
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
                                                                                                                                                                  Local Similarity
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12.3%; Score 267; DB 4; Length 372;
25.1%; Pred. No. 2.6e-14;
tive 60; Mismatches 174; Indels 44; Gaps
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TELECOMMUNICATION INFORMATION:
                        TELEPHONE: 732-594-1958
TELEFAX: 732 594-4720
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                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                      INFORMATION FOR SEG 1D NO:
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QUADET PWEHETQETGEGVE Perfect score.

MINUSEAHLHEAGGILLPSDSQ Sequence.

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Scoring table:

122226 seqs, 20178551 residues Searched:

Gapop 10.0 , Gapext n s

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Minimum DB seq length. A Maximum DB seq length. 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum March O%

Database :

Published Applications AA:*

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| cgn2_6/prodata/2/pubpaa/USOB_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/USOF_NEW_PUB_pep:*
| cgn2_6/prodata/2/pubpaa/USOF_NEW_PUB_pep:*
| cgn2_6/prodata/2/pubpaa/USOF_PUBCOMB_pep:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No is the number of results predicted by chance to have a

SUMMARIES

Seduction Application 10, Appl	Sequence 9, April Sequence 7, April Sequence 117, April 1981 (17, April 1981)	Sequence 19, Appl Sequence 19, Appl Sequence 9, Appl. Sequence 4, Appl.	Segment of Alling Segment of A	Sequence 4, Applia detremant 4, Applia Sequence 2, Applia Sequence 2, Applia	Sequence 4, April 9 Sequence 14, Africa Sequence 14, Africa Sequence 15, Africa Sequence 1, Africa Sequence
10 US-09-966-871-80 12 US-19-939-645-89 10 US-09-803-114-21 10 US-09-804-551B-10	10 US-09-823-114-9 10 US-09-823-117-9 9 US-09-791-932-117 10 US-09-791-932-4	10 US-09-160-116-19 10 US-09-160-19 9 US-09-866-248A-8 10 US-09-170-9:9-4	10 US 09 160 116 17 10 US 09 04 761 962 20 10 US 09 826 508 6	10 US-09-885-478-4 10 US-09-897-201-4 10 US-09-930-910-2 10 US-09-879-617-2	10 US-09-789-482-4 10 US-09-823-114-19 10 US-09-823-114-19 10 US-09-885-478-28 10 US-09-885-478-28
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ALIGNMENTS

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APPLICANT: Und, Peter
APPLICANT: Und, Peter
APPLICANT: Lind, Peter
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APPLICANT: Lind, Peter
APPLICANT: Lind, Peter
APPLICANT: Bertheld
TITLE OF INVENTIN: No. 1920-0137132Alul G Fritch: Coupling
FILE PREPRING: 00145 USJ
CTEPENT APPLICATION NUMBER: 40/06
PRIOR APPLICATION NUMBER: 60/195,228
PRIOR PRILNS DATE: 2001-04-06
PRIOR PRILNS DATE: 2001-04-06
PRIOR PRILNS DATE: 2001-04-06
NUMBER OF SEO IN NOS: 10
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                                                                                                                              . Sequence 3, Application US/03913432
Patent No. USD30101131311
GENERAL INFORMATION:
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APPLICANT: ELSHOURBAGY, NABIL
APPLICANT: MIGHALOVICH, NAVIN
APPLICANT: SHABON, 18MAN
TITLE CAN INVENTION: MEGETUAR CLONING OF A GALANIN LIKE 7TM
TITLE OF INVENTION: RECEPTOR (AXOR40)
                                                                                                                                                                                                                                                                                             FILE REFERENCE: GP-70649-CL
CURPERT APPLICATION NYMBER 113/09/766,693
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PRIOR APPLICATION NUMBER: HS 09/417,170
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Parent No. US20010016337A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Berhold, Malin
APPLICANT: Berhold, Malin
TITLE CE INVENTION "COSCOLD137132A1c1 G Protein Top Led Ferrytein
FILE REFERENCE: 00.04 k.u. USECOLD137132A1c1 G Protein Top Led Ferrytein
FILE REFERENCE: 00.04 k.u.s
CURRENT APPLICATION NUMBER: US/09/828,432
CURRENT APPLICATION NUMBER: US/04.c46
PRIOR APPLICATION NUMBER: G/251,313
PRIOR PILING DATE: 200c.04.n6
PRIOR APPLICATION NUMBER: G/251,313
PRIOR PILING DATE: 200c.04.n6
RIGHT APPLICATION NUMBER: G/251,313
NUMBER OF SEQ ID NOS: 10
SOFTWARE PREENTS VORSION 3.0
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APPLICANT: Glucksmann, Maria
APPLICANT: Glucksmann, Maria
APPLICANT: Meyers, Racha,
TITLE OF INVENTION: METHOD, AND CONTOUTIONS FIRMAN I
FILE FERBRUCE: 3015% 2004, 00
CUPRENT APPLICATION NUMBER: US (10/000,960
PRIOR APPLICATION NUMBER: US An/242,040
                                                      Sequence 2, Application UG/09828432; Patent No. US20020137332A1; GENERAL INPORMATION:
APPLICANT: Vogeli, Gabriel
APPLICANT: Lind, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 5, Application US/10080960
; Publication No. US20020197695A1
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US-09-828-432-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 09 828-432-2
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260 WHILFAAG AFO-3FI -ALSQVIMFSISSANFIERWSEERFESTERWEWELLERFF 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 ---IWTVASLLPLPEWFFSTIRHHEGVE-MCLVDVPAVAEEFMSMFGKLYPL -LAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 12.4%; Score 269; DB 9; Length 349; Local Similarity 28.3%; Prod. No. 2.16 15; es 87; Conservative 54; Mismatches 128; Indels
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ONDA, Haruo
TITLE OP INVENTION GALANIN RECEPTOF PROTEIN.
NUMBER OF SEQUENCES: 17
CURPENT APPLICATION DATA:

APPLICATION BATA:

APPLICATION NUMBER -

FILING DATE: 04 MAR - 202

CLASSIFICATION: «Unknown»

FRICE APPLICATION AUGUS

APPLICATION NUMBER: 13/03/640,650

FILING DATE: 11-OCT-1995

APPLICATION NUMBER: 7 134412

FILING DATE: 31 MAY-1995

APPLICATION NUMBER: 6 326510

FILING DATE: 32 DEC-1994

APPLICATION NUMBER: 6 247509

FILING DATE: 13-OCT-194

ATTONNEY/AGENT INFORMATION:

MAKER: RESHICK, DAVID S

PREFFRENCE/POCKET NUMBER: 4 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino acid
TOPCIG3Y: Linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-090-569-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMINICATION INFORMATION:
TELETHINE: 617 523 3400
TELEFAX: 617-523-6440
INFURMATION FOR SEY ID NO. 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Sequence 5, Application US/10090569
/ Publication No. US20030008329A1
/ GENERAL INFORMATION:
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HOSOYA, Masaki
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FUKUSUMI, Shoji
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 87, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 348
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ONDA, HATUO
TITLE OF INVESTITA SALAHIH PETEPPOP (POCETH, (POCUTION AND USE THEPETE
NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KVCFMYASDPAKQVSIHNYTIWSVLVAIWTVASLLPLPEWFPSTIRHHEGVEMCLVDVPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 HSLILMLSLADLSLLLFSAPIPATAYSFSVWDIGWFV″FSSDWFIHT″MAAFSITIVVVA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KUCPMYASDPAKQUSIRRYTIMSVLVAIWTVASLLFLFEWFFSTIRHHEGVEMCLVDVFA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 9%, Serre 2005, 28 %, Length 461,
100 0%; Pred, No 8.7e-167;
Live 0; Mismatches 0; Indels
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PRIOP FILING PATE: 2000 10-20
PRIOP APPLICATION NUMBER: 10 KG/242,039
PRIOR APPLICATION NUMBER: US 60/241,992
PRIOR PILING DATE: 2000 10-20
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COMPUTER: IRM Compatible
OPERATING SYSTEM: POS
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STREET: 130 WATER STREET
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Publication No. US20030008129A1
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OHTAKI, Tetsuya
HOSOYA, Masaki
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US-10-080-960-5
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Publication No. US20020194657A1
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Best Local Similarity 24.5%;
Matches 101; Conservative
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OPGANISM: Mus musculus
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                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 WFVCKSSDWFIHTCMAAKSLTIVVVAKVCFMYASDPAKQVSI-HNYTIWSVLVA----- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 ---IWTVASLLPLPEWFFSTIRHHEGV.-----EMCLVDVPAVAEEFMSMFGKLYPL- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 LARES TELEFERSETERRATIONEPERSONERSCHENGISSELVANGUSTALUSALLWUF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 TEVESTILIPITALOFOYARVINELHER-IENMSPREBASEPETAGTVLVVVVEGISKUP 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 EWVANTWIWWILKAAGPAPPPOGFI - ALSQVIMFSISSAMPLIFLVMSEEPPESLYGVWKW 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 HHIIHIWAEF--GVFDLTPASFLFPITAHCLAYSNSSWNPIIYAFLSENFRYAYFQVFKC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 AFICK----FIH-----YFFTVSMLVSIFTLAAMSVDPYVAIVHSPRSSSLPVSPNALLG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 VGTIWALSTAMASP-----VATHQATEHPPASNQTFAWEQWPPPPHK-----KAYVV(1 40)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK VÖFVGNIGVIGILIJHNAWKGKP-SMIHSLILNESLADISLILFSAPIRATAYSKSVWDLG 94
                ADDRESSEE TIKE, BRONSTEIN, FORESTS & OLSHMAN
STREET: 130 WATER STREET
CITY, EOSTON
                                                                                                                                                                                                                                                                                                APPLICATION NUMPER 83/10/090,369 FILING DATE: 04-Mar-2002 CLASSIFICATION: chassification:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/540,650
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TELECOMMUNICATION INFORMATION.
                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 1 5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 6-326610
FILING DATE: 28-DFC-1994
APPLICATION NUMBER: 6-247599
FILING DATE: 13-OFT-1994
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APPLICATION NIMBER 7-134412
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                                                                                                                                                                                MEDIUM TYPE, Diskette
COMPUTER: IRM Comparible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                               COMPITTED PEADABLE FORM.
COPPESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear
MOLECULE TYPE: Peptide
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APPLICANT: Felsch, Jason S.
APPLICANT: Felsch, Jason S.
APPLICANT: Annis, David Allen
APPLICANT: Ansis, David Allen
APPLICANT: Ansh, Huw M.
TITLE OF INVENTION. Affinity Selection Baned Servering of By Herlib Form.
FILE REFERENCE: 110.02, 173 US2
FURBERT: 110.02, 173 US2
FURBERT: LIGHT AFLICATION NUMBER: WS 40/258,970
PRIOR APPLICATION NUMBER: US 60/258,970
NUMBER OF SEC ID NOS: 34
SSPTWARE: FastSep for Windows Version 4.0
SEC ID NO 9
APPLICANT: Allen, Keith D.
TITLE OF INVENTION. TRANSCENIC MICE CONTAINING
TITLE OF INVENTION. TRANSCENIC MICE CONTAINING
TITLE OF INVENTION. SIGNCCCORTIONS INVENTION PROPERTY FROM THE OFFICE PROPERTY FROM THE OFFICE PROPERTY FROM THE OFFICE PROPERTY FILTING FATE: 1000-07-10
PRIOR APPLICATION NUMBER: US 6/217,179
PRIOR APPLICATION NUMBER: US 6/312,299
PRIOR FILING FATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/322,299
PRIOR FILING FATE: 2000-11-20
PRIOR FILING FATE: 2001-01-16
NUMBER OF SEQ IN NOS.
SOFTWARE: FASUSE 2001-01-16
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24.5%; Pred. No. 1.5e lu;
"Ye - 60; Migmatchos 274; Defete ---, Lapt
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                                                  257 PROHFTYHITVHILVYCFPELIMGHTYTIVGITLWGGELFGOTÖPK -
                                                                                                                                              PROTECTION PROGRAMMENT OF PRINCE INTROPREMENT
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PRIOR APPLICATION NUMBER: Japan 8-021562
FILING DATE: 2-JUL-1996
ATTOENEY/ASEN INFOFMATION:
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CURRENT APPLICATION DATA.
APPLICATION NUMBER 18/08/796,570A
FILING DATE: 06.FEB-1997
                                                                                                   233 KQVTVMLLSIAIIS-ALLWLPEWV-----
                                                                                                                                                                                                                                                                                                                                                                 PATIMENT 1, AFETTATION USCOMMENTAL OBJECT NO. USSOMMENTON: GENERAL INFORMATION: GENERAL INFORMATION:
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FEGISTRATION NUMBER: 30,628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 Water Street
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617.523-6440
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  192 AEEFMS.
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US-08-796-570A-1
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APPLICANT: Annis, David Allen
APPLICANT: Kaldhatgi, Krishna
APPLICANT: Mash, Huw M
TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins
FILE REFERENCE: 111025-173-173
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                                                                                                                       10-3%; Score 224; DB 4; Length 488;
23.6%; Fred. No. 2 14-11;
tive - 62; Mismatches 133; Indels 58; Gaps
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                                                                                                                                                                                                                   16 PSDSQDWRTII-----PALLVA------VCLVGFVGNJCVIGILLHNAWKGKPSMIHS 62
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"IMPRIT FILING PATE: 20.7 0.2 2
PPIOP APPLICATION NUMBER: US 60/258,970
PPIOP APPLICATION NUMBER: US 60/258,970
NUMBER OF SEQ ID NOS- 34
SOFTWARE: FASESEQ for Windows Version 4.0
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// Patent No. US20020164617A1
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Best Lical Similarity 23.6%,
...ches 78; Conservative
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ORGANISM: Human
                                             ORGANIOM. Human
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                                                             US-10-029-009-9
LENGTH: 488
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                         TYPE: FRT
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Post Total Similarity 20.2%, Pred. No. 9.26-11;
Matches 95, Conservative 65, Mismatches 159, Indeis 179, July
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9.9%, Stile DIS.S., Dength 413,

Best Local Similatity 22.2%, Prod No. 9.2e-11,

Matcher 95, Connermative 61, Mismatches 119, Infels 129, Gapo
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G Protein Coupled Receptor Proteins, TITLE OF INVENTION. Their Production And Use NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS: A FERTILE. Tike, Brintein, Rüberte & Cushman, LLF STREET: 130 Water Street.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-FEB-1997
AFFLICATION HUMBER: Japan 9.21562
FILING DATE: 2-JUL-1996
ATTOCHET/ADENT INFORMATION:
NAME: BISENSEEIN, RORALD I.
REGIOTEATION HUMBER: 30,628
REFERENCE/CONT HUMBER: 47147
TELECOMMUNICATION HUMBER: 47147
TELECOMMUNICATION HUMBER:
TELEDHONE: 617-523-4400
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APPLICATION NUMBER. UC/10/06.477
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                                                    184 FF-----MSMFGKLYPLLAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRS---KQV 235
                                                                                                       204 SWPLAHHPTIYTTFLILIFQYCLPLGFILVCYAPIYPPLQRQGRVFHKGTYSLPAGHWFQV 263
                                                                                                                                                            236 TVMLLSIAIISALLWLPEWV AWLWVWHLKAAGPAPPOGPIALSOVLMFSISSANFLIFL 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 AFG -- LPL FFASFYFWRAYDQCFYRFG -- TKTQNLRNQIPSKQVTVMLLSTAI 244
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145 NPTGWPPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHROMSKALEF-LABRYVCTE 203
                                                                                                                                                                                                                 264 NVVLVVVVVAFAVLWLFLHVFNSLEDWHHEAIFICHGNLIFLVCHLLAMASTCVNFFIYG 323
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| Barent No. US20023111473A1

| GENERAL INFORMATION:

| APPLICANT: ASJTAWY, Roman L.

| APPLICANT: MCMHINIE, Elizabeth A.

| TITLE OF INVENTION: No. US20020111473A101 G Frotein Coupled Receptor

| FILE REFERENCE: 9074-9004
                                                                                                                                                                                                                                                                295 UNGEEFPRGLEAWWWYTTEPPFUSESOETPAGNSEGIE 334
                                                                                                                                                                                                                                                                                                                        324 FLNTNFKKEIKAL------VLTCOOSAPLEESEHLP 353
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EARLIER FILING DATE: 1909-04-16
EARLIER FILING DATE: 1909-04-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN Ver. 2.0
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CUPPENT FILING DATE: 1999-04-16
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US-09-292-973-2
US-09-292-973-2
; Patent No US20020111473A1
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Bost Local Similarity 24.5%; Pred. No. 6.7e-10;
Matches 91; Conservative 54; Mismatches 170; Indels 57; Japa
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APPLICANT: ZASTAWAY, Roman L.
APPLICANT: WOWHINNIE, Eliaabeth A.
TITLE OF INVENTION WS 482 002114778; d. Fritzin Coupled Reception
FILE PEPEPROCH 404 4094
CUPPENT APPLICATION NUMBER: US/09/202,973
CUPPENT APPLICATION NUMBER: US/09/202,973
CUPPENT FILING PAIE: 1999-04-16
EAPLIER PILING PAIE: 1998-04-16
NUMBER OF SEQ ID NOS: 20
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TILLE OF INVENTION. CELTA OFFICIO AND METHODS RELATING THERETOFFILE OF INVENTION. COMPOSITIONS AND METHODS RELATING THERETOFFILE OF INVENTION. COMPOSITIONS AND METHODS RELATING THERETOFFICE PROFICATION NUMBER: US/10/112, 599A
TOUR PENT FILLING DATE. 2020:09 05
PITOP APPLICATION NUMBER: US 60/280,513
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Best Local Similarity 23.8%; Pred. No. 8.1e-10;
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